JE17 Rec'd PCT/PTO 2 6 APR 2001 Customized FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE ATTORNEY DOCKET NO. P07180ÚS00/BAS TRANSMITTAL LETTER TO THE UNITED STATES U.S. APPLICATION NO DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371 INTERNATIONAL APPLICATION NO. INTERNATIONAL FILING DATE PRIORITY DATE CLAIMED PCT/FR99/02643 28 October 1999 30 October 1998 TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES SPECIFIC OF THE NEISSERIA GENUS ... * APPLICANT(S) FOR DO/EO/US: AUJAME et al. Applicant herewith submits to the US Designated/Elected Office (DO/EO/US) the following items and other information: This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 USC 371... 3. This express request to begin national examination procedures (35 USC 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 USC 371(b) and PCT Art. 22 and 39(1). 4. A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date. A copy of the International Application as filed (35 U.S.C. 371 (c)(2)) a. is transmitted herewith (required only if not transmitted by the International Bureau). b. has been transmitted by the International Bureau. X c. is not required, as the application was filed in the United States Receiving Office (RO/US). A translation of the International Application into English (35 U.S.C. 371(c)(2)). 7. Amendments to the claims of the International Appln, under PCT Article 19 (35 USC 371 (c)(3)) a. are transmitted herewith (required only if not transmitted by the International Bureau). b. have been transmitted by the International Bureau. c. have not been made; however, the time limit for making such amendments had NOT expired. d. have not been made and will not be made. 8. A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).

9. An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).

10. A translation of the annexes to the Int'l Prelim. Exam. Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 20. below concern document(s) or information included: 11. An Information Disclosure Statement under 37 C.F.R. 1.97 and 1.98.

12. An Assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.

13. A First preliminary amendment.

14. A Second or Subsequent preliminary amendment.

15. A substitute specification.

16. A change of power of attorney and/or address letter.

17. A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 & 35 USC 1.821-825.

18. A second copy of the published international application under 35 USC 154(d)(4).

19. A second copy of the English translation of the international application under 35 USC 154(d)(4).

20. Other items or information:

A copy of the Notification of Missing Requirements under 35 U.S.C. 371.

In the event that a petition for extension of time is required to be submitted herewith, and in the event that a separate petition does not accompany this response, applicant hereby petitions under 37 CFR 1.136(a) for an extension of time of as many months as are required to render this submission timely. Any fee is authorized in 17(c).

Date: April 26, 2001

U.S. APPLICATIO	30433	NO. A	TTORNEY DOO P07180US00			
X 21. The following	ng fees are submitted	l:			CALCULATION	NS PTO USE ONLY
X Basic National	Fee (37 CFR 1.492 (a) (1)-(5):		i		
Neither Int'l	Prelim. Exam. fee no	r Int'l Search fee paid	to USPTO	\$1000		
X Search Repor	rt has been prepared b	y the EPO or JPO		\$ 860		•
☐ No Int'l Prelim	n. Ex. fee paid to USPT	O but Int'l Search fee pa	aid to USPTO	\$ 710		
☐ International	preliminary examinat	tion fee paid to USPT	РО	\$ 690	7	· •
Int'l Prelim. E	x. fee paid to USPTO &	all claims satisfied PC	T Art. 33(1)-(4	\$ 100	٠,	
	ENTER .	APPROPRIATE BA	SIC FEE A	MOUNT =	\$ 860.00	
	30 for furnishing the claimed priority date		er than	20 mos. +	\$	
CLAIMS	NUMBER FILED	RATE				
Total Claims	- 20 =	\$18 =	\$			
Independent Claims	- 03 =	\$80 =	\$			
☐ Multiple Depend	lent Claim(s) (if appli	\$270 =	\$			
		ATIONS =	\$ 860.00			
Applicant claims	s small entity status. S	See 37 CFR 1.27. The	fees indicate	ed -	\$	
			SUI	STOTAL =	\$ 860.00	
	\$130 for furnishing the laimed priority date (37)		er than	20 mos. +	\$	
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	the enclosed assignmen n appropriate cover shee				\$	
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1.137(a) or (b)) must be filed and					ive (37 CFA
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B. Aaron S		GNATURE:		r 5. poh	191	
,	v) of CUSTOMER N	*''	AME: Dougl	as E. Jackson	•	
	I & TAYLOR, PI RTH FAIRFAX S		EG. NO.: 28,	518		
SUITE 90		PF	HONE NO.: 7	703-739-4900)	
	IDRIA, VA 2231	2001				

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re patent application of: AUJAME et al.

Serial No.: 09/830.433

Examiner:

Filed: April 26, 2001

Art Unit:

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC

Docket No.: P07180US00/BAS

OF THE NEISSERIA GENUS...

PRELIMINARY AMENDMENT

Honorable Commissioner for Patents

Washington, DC 20231

SIR:

In response to the Notice dated December 6, 2001, please amend the application as follows:

IN THE SPECIFICATION:

After Page 49, please substitute the attached Sequence Listing for any Sequence Listing previously filed in the application.

REMARKS

By this Preliminary Amendment, Applicants are submitting a revised Sequence Listing which overcomes the objections pointed out in the Notice dated December 6, 2001, as well as a copy of the paper sequence in computer readable form.

STATEMENT UNDER 37 CFR § 1.821

Applicants hereby certify in accordance with 37 C.F.R. 1.821(f) that the content of the enclosed paper sequence listing and computer readable form of the sequence listing are the same. In accordance with 37 C.F.R. 1.821(g), Applicants hereby certify that the enclosed submission contains no new matter.

In light of the foregoing, it is submitted that all prior objections have been overcome, and that the present application should be examined and passed on to allowance at the earliest possible time.

Respectfully submitted,

LARSON & TAYLOR, PLC

Date: February 5, 2002

Transpotomac Plaza 1199 N. Fairfax Street Suite 900 Alexandria, VA 22314 (703) 739-4900 B. Aaron Schulman Registration No. 31,877

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent

In repatent application of: AUJAME et al.

Serial No.: 09/830.433

Examiner:

Art Unit:

Filed: April 26, 2001

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC

Docket No.:

OF THE NEISSERIA GENUS...

P07180US00/BAS

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents Washington, D.C.

SIR:

Prior to examination, please amend the above-identified application as follows.

IN THE SPECIFICATION:

After page 49, please insert the enclosed Sequence Listing as a substitute for the one filed in the original application.

IN THE CLAIMS:

A clean version of the amended claims is provided herewith in Attachment A. It will be noted that the claims have been amended relative to the previously provided version as shown by the marked up version thereof in Attachment B provided herewith.

REMARKS

By this Amendment, the claims have been rewritten to reduce the multiple dependencies. In addition, in response to the Notice to Comply with the sequence listing requirements, a computer readable form and paper copy of the Sequence Listing is now provided, and Applicants state that the paper copy and computer readable form are identical and add no new matter to the application.

Examination and allowance of the present application is thus earnestly solicited.

Respectfully submitted,

Date: 16 August 2001

B. Aaron Schulman Registration No. 31,877

LARSON & TAYLOR PLC Transpotomac Plaza 1199 North Fairfax Street, Suite 900 Alexandria, Virginia 22314 (703) 739-4900

ATTACHMENT A

Clean Replacement/New Claims

Following herewith is a clean copy of each claim which replaces each previous claim having the same number and each new claim.

- (Amended) Expression vector comprising an expression cassette in which
 a nucleotide sequence as defined in Claim 1 is placed under conditions allowing its
 expression in a host cell.
 - 9. Canceled.
- (Amended) Monospecific antibody directed against a polypeptide according to Claim 5.
- 11. (Amended) Use of a nucleic acid according to Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.
- 12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

- 13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.
- 14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

ATTACHMENT B

Marked Up Replacement Claims

Following herewith is a marked up copy of each rewritten claim.

- (Amended) Expression vector comprising an expression cassette in which
 a nucleotide sequence as defined in ene of Claime 1 to 4 Claim 1 is placed under
 conditions allowing its expression in a host cell.
 - Canceled.
- 10. (Amended) Monospecific antibody directed against a polypeptide according to either of Claims 5 and 6 Claim 5.
- 11. (Amended) Use of a nucleic acid according to enc of Claime 1 to 4 Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, according to either of Claime 5 and 6, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.
- 12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

- 13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.
- 14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

130

<110> AUJAME et al.

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140

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	gta Val															624
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85

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 Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
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912

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Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala 35 40

Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val 50 60

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg 65 75 80

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala 85 90 95

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly 115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr $130 \,$ $135 \,$ $140 \,$

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu 145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp 165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu 180 185 190 Ala Gly Asp Val Leu. Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp 280 Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu 295 Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu 315 Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu 345 Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu 375 380 <210> 15 <211> 717 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(714) <400> 15 atg aat aga eec aag caa eec tte tte egt eec gaa gte gee gtt gee Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga ccg ttg tca Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser ttt tcc cta tgg acg aca ttt gca tcg ata tct gcg tta ttg att atc 144 Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192 Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly caa att tta cct gca tcg ggc gta atc agg gtg tat gca ccg gat acg

240

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cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe

gaa atg ege tet gaa caa ate ate egt gea gga egg teg ggt tat ata 240 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr. Ile

gca ata eeg aac gte gaa gte gga eag eag gtt gat eet tee aaa etg Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu

ctc ttg age att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat 336

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cac gag aaa d His Glu Lys i 210	egg egg Arg Arg	Leu 1	tac ga Fyr Gl 215	a tgg .u Trp	gta Val	ttg Leu	gag Glu 220	ctg Leu	att Ile	tat Tyr	agt Ser	672
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Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser 150 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val 165 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser 215 Met Ser Gly Lys Leu 225 <210> 19 <211> 1743 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(1740) <400> 19 atg aaa ttt ttt cct gct cca tgt ctg ttg gtt atc ctg gct gtc ata Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile ccc ctt aaa acc tta gct gcc gat gaa aac gat gca gaa ctt atc cgt Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg tcc atg cag cgt cag cac ata gat gct gaa ttg tta act gat gca Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala 4.0 aat gtc cgt ttc gag caa cca ttg gag aag aac aat tat gtc ctg agt Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser gaa gat gaa aca eeg tgt act egg gta aat tae att agt tta gat gat 240 Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp aag acg gcg cgc aaa ttt tct ttt ctt cct tct gtg ctc atg aaa gaa 288 Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu 90 aca gct ttt aaa act ggg atg tgt tta ggt tcc aat aat ttg agc agg 336 Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg cta caa aaa gcc gcg caa cag ata ctg att gtg cgt ggc tac ctc act 384 Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr

too caa got att atc caa coa cag aat atg gat tog gga att otg aaa

432

Ser	Gln 130		Ile	Ile		Pro 135	Gln	Asn	Met	Asp	Ser 140	Gly	Ile	Leu	Lys	
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			aag Lys													528
			tat Tyr 180													576
ggc Gly	ttg Leu	gaa Glu 195	aac Asn	ctg Leu	cgt Arg	cgt Arg	ttg Leu 200	ccg Pro	agt Ser	gtt Val	aaa Lys	aca Thr 205	gat Asp	att Ile	cag Gln	624
			tcc Ser													672
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ggc Gly	aaa Lys	acg Thr	acc Thr	ggc Gly 245	aaa Lys	tat Tyr	caa Gln	gga Gly	aat Asn 250	gtc Val	gct Ala	tta Leu	tcg Ser	tcc Ser 255	gat Asp	768
			ggc Gly 260													816
ttg Leu	gtg Val	cac His 275	aaa Lys	acg Thr	gac Asp	ttg Leu	act Thr 280	gct Ala	gcc Ala	acc Thr	ggt Gly	acg Thr 285	gaa Glu	act Thr	gaa Glu	864
			aga Arg													912
			tct Ser													960
			tcc Ser													1008
			gcc Ala 340													1056
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gaa Glu 385	ttg Leu	cgc Arg	cac His	cgt Arg	gct Ala 390	tac Tyr	ctc Leu	cac His	cgt Arg	tgg Trp 395	cag Gln	ctt Leu	gac Asp	ggc Gly	aag Lys 400	1200

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														ctt Leu		1680
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Ser	Met	Gln 35	Arg	Gln	Gln	His	Ile 40	Asp	Ala	Glu	Leu	Leu 45	Thr	Asp	Ala	
Asn	Val	Arg	Phe	Glu	Gln	Pro	Leu	Glu	Lys	Asn	Asn	Tyr	Val	Leu	Ser	

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys 135 Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly 265 Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu 280 Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys 295 Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp 360

Ser 31 Arg Met bys Leu 1rp inr Arg Gin inr lyr bys 17 lie Asp 355

Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala 370

Glu Leu Arg His Arg Ala Tyr Leu His Arg Trp Gln Leu Asp Gly Lys 385

390

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro

405 Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile Ile Thr Ala Gly Leu Asp Ala Ala Pro Ser Met Leu Gly Lys Gln 440 Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro 455 Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp 490 Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu 505 Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys 535 Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu 570 Asn Tyr Ser Phe <210> 21 <211> 411 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(408) <400> 21 atg att gaa ttt gtc cga gcc aaa aaa cgg ctg ctt tgg gca ttt gtg

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gaa gcg aaa caa acc gcc ctg att gcc acc tat cgg cat tct tct atg 144 Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met 40

192 gtt geg geg gaa caa tac gec ttg cag ett aaa aaa geg cag gae gaa Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu

agg cag egg tgg tac gac ttt tee caa aaa caa gga aga aag eee gtg 240 Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val 75 70

aaa aaa cag tat cog, cog caa acg aaa aaa goo ggo tat ctg aaa acc Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln 120 aaa gaa cgc aac tcg tcg cag ggt taa 411 Lys Glu Arg Asn Ser Ser Gln Gly <210> 22 <211> 136 <212> PRT <213> Neisseria meningitidis <400> 22 Met Ile Glu Phe Val Arg Ala Lys Lys Arg Leu Leu Trp Ala Phe Val Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln Lys Glu Arg Asn Ser Ser Gln Gly <210> 23 <211> 924 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(921) <400> 23 atg caa tac agc aca ctg gca gga caa acc gac aac tcc ctc gtt tcc 48 Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser 10

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agt Ser	cat His	gcc Ala 35	gat Asp	tgg Trp	gtt Val	att Ile	acc Thr 40	ggc Gly	gtg Val	cct Pro	tat Tyr	gat Asp 45	atg Met	gcg Ala	gtt Val	144
tca Ser	ggg Gly 50	cgt Arg	tcc Ser	ggc Gly	gcg Ala	cgt Arg 55	ttc Phe	ggt Gly	cct Pro	gaa Glu	gcc Ala 60	atc Ile	cgg Arg	cgc Arg	gcc Ala	192
tcc Ser 65	gtc Val	aac Asn	ctc Leu	gct Ala	tgg Trp 70	gag Glu	cac His	ege Arg	agg Arg	ttt Phe 75	cca Pro	tgg Trp	aca Thr	ttt Phe	gat Asp 80	240
gtg Val	cgc Arg	gaa Glu	ege Arg	ctg Leu 85	aac Asn	att Ile	att Ile	gat Asp	tgc Cys 90	ggc Gly	gac Asp	ttg Leu	gtt Val	ttt Phe 95	tct Ser	288
ttt Phe	ggc Gly	gac Asp	agc Ser 100	agg Arg	gat Asp	ttt Phe	gtc Val	gaa Glu 105	aaa Lys	atg Met	gaa Glu	gcg Ala	cac His 110	gcc Ala	ggc	336
		ctt Leu 115														384
		acc Thr														432
		ctg Leu														480
agc Ser	gaa Glu	tac Tyr	gac Asp	cac His 165	ggt Gly	acg Thr	atg Met	ttc Phe	tat Tyr 170	acc Thr	gcc Ala	ccc Pro	aag Lys	gaa Glu 175	ggc Gly	528
		gac Asp														576
agt Ser	aaa Lys	aaa Lys 195	ttg Leu	cct Pro	ttt Phe	act Thr	gtg Val 200	ttg Leu	acc Thr	gcc Ala	ccc Pro	caa Gln 205	gtt Val	aat Asn	gaa Glu	624
		gtt Val														672
atg Met 225	ccc Pro	gtt Val	tac Tyr	ctg Leu	act Thr 230	ttc Phe	gac Asp	ata Ile	gac Asp	tgc Cys 235	ctc Leu	gac Asp	ccg Pro	tcg Ser	ttc Phe 240	720
gcc Ala	ccc Pro	ggg Gly	acc Thr	ggt Gly 245	acg Thr	ccc Pro	gta Val	tgc Cys	ggc Gly 250	ggc Gly	ttg Leu	agc Ser	agc Ser	gac Asp 255	agg Arg	768
gca Ala	tta Leu	aaa Lys	atc Ile 260	cta Leu	cgt Arg	ggg Gly	ctg Leu	acg Thr 265	gat Asp	ctc Leu	gac Asp	atc Ile	gtc Val 270	ggt Gly	atg Met	816
gat	gtt	gta	gaa	gtt	gcc	ccc	tct	tac	gac	caa	tcc	gac	att	acc	gct	864

Asp V		Val 275	Glu		Ala	Pro	Ser 280	Tyr	Asp	Gln	Ser	Asp 285	Ile	Thr	Ala	
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Ser H	His	Ala 35	Asp	Trp	Val	Ile	Thr 40	Gly	Val	Pro	Tyr	Asp 45	Met	Ala	Val	
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Ser V 65	Val	Asn	Leu	Ala	Trp 70	Glu	His	Arg	Arg	Phe 75	Pro	Trp	Thr	Phe	Asp 08	
Val A	Arg	Glu	Arg	Leu 85	Asn	Ile	Ile	Asp	Суs 90	Gly	Asp	Leu	Val	Phe 95	Ser	
Phe (Gly	Asp	Ser 100	Arg	Asp	Phe	Val	Glu 105	Lys	Met	Glu	Ala	His 110	Ala	Gly	
Lys 1	Leu	Leu 115	Ser	Ser	Gly	Lys	Arg 120	Cys	Leu	Ser	Leu	Gly 125	Gly	Asp	His	
Phe :	Ile 130	Thr	Leu	Pro	Leu	Leu 135	Arg	Ala	His	Ala	Arg 140	Tyr	Phe	Gly	Lys	
Leu <i>l</i> 145	Ala	Leu	Ile	His	Phe 150	Asp	Ala	His	Thr	Asp 155	Thr	Tyr	Asp	Asn	Gly 160	
Ser (Glu	Tyr	Asp	His 165	Gly	Thr	Met	Phe	Tyr 170	Thr	Ala	Pro	Lys	Glu 175	Gly	
Leu :	Ile	Asp	Pro 180	Ser	Arg	Ser	Val	Gln 185	Ile	Gly	Ile	Arg	Thr 190	Glu	His	
Ser 1	Lys	Lys 195	Leu	Pro	Phe	Thr	Val 200	Leu	Thr	Ala	Pro	Gln 205	Val	Asn	Glu	
Asp	Ser 210	Val	Glu	Glu	Thr	Val 215	Arg	Lys	Ile	Lys	Glu 220	Thr	Val	Gly	Asn	
Met : 225	Pro	Val	Tyr	Leu	Thr 230	Phe	Asp	Ile	Asp	Cys 235		Asp	Pro	Ser	Phe 240	
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Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
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Lys Lys Asp
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att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcg acc
Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr
gaa tat ttt qtc qta tqc ttt ctq cgt ttg atg cca ctc tct ccq tgt
                                                                   144
Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
                              40
aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcg gaa ata gaa
Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
     50
                                                                   240
aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcg
Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa
                                                                   288
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
                 8.5
                                      90
gge cag tat geg gta gea tac gae ett tee tge aag aaa gat tge cat
                                                                   336
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
            100
                                                                   384
gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct
Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
        115
                             120
gtc ccg cca ctg cac cgt cac cga aat cgc caa aca gct taa
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Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
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Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
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Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
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Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
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gea aaa aee aga gae eeg atg tgg gae aat geg get tta eag aee age
Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
         35
gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg
                                                                   192
Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
gaa tac cgc tat gtg gat gtc ctg caa ccc aac cat tcc gat att att
                                                                   240
Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
 65
cgg tat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata
Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
                  85
cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag
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His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys

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aaa too tat ttt too aaa tat ato ota ooc gtt toa ett ttt aco ttg Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu 40

cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala

tgg cgg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac

Trp 65	Arg	Ala	Ala		Gln 470	His	Ser	Ala	Asp	Phe 75	Gln	Ala	Ser	His	Tyr 80	
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ctt Leu	ccc Pro	cat His	gta Val 100	tcc Ser	gcc Ala	aat Asn	gcc Ala	agc Ser 105	tac Tyr	cag Gln	ege Arg	cag Gln	ccg Pro 110	cca Pro	tcg Ser	336
att Ile	tct Ser	tcc Ser 115	acc Thr	cgc Arg	gaa Glu	aca Thr	cag Gln 120	gga Gly	tgg Trp	agc Ser	gtg Val	cag Gln 125	gtg Val	gga Gly	caa Gln	384
acc Thr	tta Leu 130	ttt Phe	gac Asp	gct Ala	gcc Ala	aaa Lys 135	ttt Phe	gca Ala	caa Gln	tac Tyr	cgc Arg 140	caa Gln	agc Ser	agg Arg	ttc Phe	432
gat Asp 145	acg Thr	cag Gln	gct Ala	gca Ala	gaa Glu 150	cag Gln	cgt Arg	ttc Phe	gat Asp	gcg Ala 155	gca Ala	cgc Arg	gaa Glu	gaa Glu	ttg Leu 160	480
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acc Thr	gtt Val	gcc Ala	gcc Ala 180	cat His	gcg Ala	gcg Ala	gaa Glu	aaa Lys 185	gag Glu	gct Ala	tat Tyr	gcc Ala	cag Gln 190	cag Gln	gta Val	576
agg Arg	cag Gln	gcg Ala 195	cag Gln	gct Ala	tta Leu	ttc Phe	aat Asn 200	aaa Lys	ggt Gly	gct Ala	gcc Ala	acc Thr 205	gcg Ala	ctg Leu	gat Asp	624
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gcc Ala 225	gta Val	ttg Leu	gct Ala	gag Glu	aaa Lys 230	Gln	acc Thr	tat Tyr	gaa Glu	aac Asn 235	cag Gln	ttg Leu	aac Asn	gac Asp	tac Tyr 240	720
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tca Ser	tct Ser	geç Ala	cag Glr	aat Asr 325	. Asr	gac Asp	tac Tyr	cac His	tat Tyr 330	: Arc	ggc Gly	aaa Lys	ggg Gly	atg Met 335	Ser	1008

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115 120 125

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Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp $165 \hspace{1.5cm} 170 \hspace{1.5cm} 175$

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp $195 \hspace{1.5cm} 200 \hspace{1.5cm} 205$

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu \$245\$

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 260 265 270

Gln Arg Tie Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 $$ 310 $$ 315 $$ 320

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 415 \$410\$

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 420 425 430

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195

696

Pro Ser Cys Cys Ala Gln Val 225 230

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ISBNICKS. COLCE

last.

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Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala 35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly 50

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr 65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln 85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe $100 \,\,$

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe 115 \$120 \$125

Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe 180 185 190

Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln 195 200 205

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acc Thr	aaa Lys	ggg ggg	ctg Leu 20	ttg Leu	ata Ile	aac Asn	ggt Gly	tac Tyr 25	cat His	ttc Phe	acc Thr	gcc Ala	cac His 30	gcg Ala	acg Thr	96
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tct Ser 65	aat Asn	caa Gln	gga Gly	atg Met	ttg Leu 70	ggg Gly	cat His	ttt Phe	gcc Ala	aac Asn 75	gaa Glu	att Ile	tcc Ser	acc Thr	tat Tyr 80	240
gcc Ala	cta Leu	ege Arg	agc Ser	gat Asp 85	tat Tyr	ccg Pro	tgg Trp	ttt Phe	acc Thr 90	caa Gln	agg Arg	ggt Gly	gat Asp	tat Tyr 95	ggc Gly	288
aaa Lys	agc Ser	gcg Ala	ggg Gly 100	ttg Leu	agc Ser	gac Asp	cgc Arg	ctt Leu 105	ttg Leu	ttg Leu	ccg Pro	gcg Ala	ttc Phe 110	aaa Lys	cgg Arg	336
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ato	gcg Ala	caa Gln	acc Thr	gat Asp 165	aaa Lys	ttt Phe	tta Leu	gaa Glu	gat Asp 170	Thr	gtt Val	aag Lys	ata Ile	ttg Leu 175	Asn	528
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~20	~~c	+-+	an+	245 ttt	+aa	aaa	aa+	att.	250	mat	ata	can	aac	255 maa	aac	816
Asp	Gly	Tyr	Asp 260	Phe	Trp	Gly	Asn	Val 265	Pro	Asp	Val	Gln	Gly 270	Glu	Gly	
				ttt Phe												864
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Asn	Leu	Ser 35	Leu	Pro	Gln	Thr	Leu 40	Gly	Leu	Pro	Gly	Glu 45	Pro	Asn	Asn	
Asn	Ile 50	Val	Ser	Leu	Ala	Lys 55	Gln	Ala	Gly	Phe	Arg 60	Thr	Ala	Trp	Leu	
Ser 65	Asn	Gln	Gly	Met	Leu 70	Gly	His	Phe	Ala	Asn 75	Glu	Ile	Ser	Thr	Tyr 80	
Ala	Leu	Arg	Ser	Asp 85	Tyr	Pro	Trp	Phe	Thr 90	Gln	Arg	Gly	Asp	Tyr 95	Gly	
Lys	Ser	Ala	Gly 100	Leu	Ser	Asp	Arg	Leu 105	Leu	Leu	Pro	Ala	Phe 110	Lys	Arg	
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Leu	Met 130	Gly	Ser	His	Ser	Asp 135	Phe	Cys	Thr	Arg	Leu 140	Asp	Lys	Asp	Ala	
Arg 145	Arg	Phe	Gln	Tyr	Gln 150		Glu	Lys	Ile	Ser 155	Cys	Tyr	Val	Ser	Thr 160	
Ile	Ala	Gln	Thr	Asp 165	Lys	Phe	Leu	Glu	Asp 170	Thr	Val	Lys	Ile	Leu 175	Asn	
Glu	Asn	Lys	Glu 180	Ser	Trp	Ser	Leu	Val 185	туг	Phe	Ser	Asp	His 190	Gly	Leu	
Met	His	Val 195	Gly	Lys	Gly	Gly	Glu 200	Arg	Thr	Leu	Thr	His 205	Gly	Ala	Trp	
Lys	Arg 210		Ser	Tyr	Gly	Val 215	Pro	Leu	Val	Lys	11e 220	Ser	Ser	Asp	Asp	
Thr	Ara	Ara	Glu	Met	Ile	Lys	Val	Arq	Arg	Ser	Ala	Phe	Asn	Phe	Leu	

CONTON CATOO

Arg Gly Phe Gly Ser Trp Thr Gly Ile Glu Thr Asp Glu Leu Pro Asp $245 \hspace{1cm} 250 \hspace{1cm} 255 \hspace{1cm}$

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cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc $\,$ 144 Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly $\,$ 35 $\,$ 40 $\,$ 45

ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca 192 Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr 50 60

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acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat 288 Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn of as

att gcc ogt acc att cgc aac ttt gaa cgc gcc ggt gtt gca gcg gtt 333 Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val

cac atc gas gat cag gta gcg cas asa cgc tgc ggc cac cgt ccg asc 384 His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn 115 120 125

aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc 432 Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala 130 1450

gta gat gcg cgc gtt gat gag aac ttc gtg att atg gcg cgt acc gat Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp 150 155 160

gcg ctg gcg gta ga Ala Leu Ala Val-Gl 16	ı,Gly Leu	gat go Asp A:	cc gct la Ala 170	atc g Ile G	gaa ege Glu Arg	gcc Ala	caa Gln 175	gct Ala	528
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gcg aac att acc ga Ala Asn Ile Thr Gl 210	g ttt ggt u Phe Gly 215	Ser T	ct ccg hr Pro	Leu T	at acc Tyr Thi	caa Gln	agc Ser	gag Glu	672
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cgt gca gca agc aa Arg Ala Ala Ser Ly 24	s Ala Ala	ctg a Leu A	at gtt sn Val 250	tac ç Tyr G	gaa gco Slu Ala	g att i Ile	atg Met 255	cgc Arg	768
gat ggc act tca gg Asp Gly Thr Ser Gl 260	c ggc ggt y Gly Gly	Gly G	ga cag Sly Gln :65	tat o	gca aa Ala Asi	e eeg n Pro 270	tgc Cys	cga Arg	816
get gta ega gea te Ala Val Arg Ala Se 275	t gaa cta r Glu Lev	tca t Ser C 280	gc ctt Cys Leu	cga q Arg <i>I</i>	gca aa Ala Ly 28	s Thr	gga Gly	taa	864
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Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp , , 1,50 Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala 165 Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu 200 Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu 215 Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe 230 Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg 250 Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly 280 <210> 37 <211> 921 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(918) <400> 37 atg cct tcg agc aaa aac tgg ata aat tgt ttc aaa aat gat tta ccg Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro ett tea gae tge ett tea aca aat eeg eat egg teg tet gaa aac eeg Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro aaa ccc ata aaa aca caa agg aga aat acc atg act gaa act act caa Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln 40 acc ccg acc ctc aaa cct aaa aaa tcc gtt gcg ctt tct ggc gtt gcg Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala gee ggt aat acc get ttg tgt acc gtt gge egt acc gge aac gat ttg Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu 288 age tat ege ggt tae gae att etg gat ttg gea caa aaa tgt gag ttt Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe gaa gaa gtt gcc cac ctg ctg att cac ggc cat tta ccc aac aaa ttc Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe 105 100

gag Glu	ctg Leu	gcc Ala 115	got. Ala	tat, Tyr	aaa Lys	gcc Ala	aag Lys 120	ctc Leu	aaa Lys	tcc Ser	atg Met	cgc Arg 125	ggc Gly	ctg Leu	cct Pro	384
Ile	cgt Arg 130	gtg Val	att Ile	aaa Lys	gtt Val	ttg Leu 135	gaa Glu	agc Ser	ctg Leu	cct Pro	gca Ala 140	cat His	acc Thr	cat His	ccg Pro	432
atg Met 145	gac Asp	gtg Val	atg Met	cgt Arg	acc Thr 150	ggc Gly	gta Val	tcc Ser	atg Met	ctg Leu 155	ggc Gly	tgt Cys	gtt Val	cat His	cct Pro 160	480
gaa Glu	cgt Arg	gaa Glu	ggc Gly	cat His 165	ccg Pro	gaa Glu	agc Ser	gaa Glu	gcg Ala 170	cgc Arg	gac Asp	att Ile	gcc Ala	gac Asp 175	aaa Lys	528
ctg Leu	atc Ile	gcc Ala	agc Ser 180	ctc Leu	ggc Gly	agt Ser	atc Ile	ctc Leu 185	ttg Leu	tac Tyr	tgg Trp	tat Tyr	caa Gln 190	tat Tyr	tcg Ser	576
cac His	aac Asn	ggc Gly 195	aaa Lys	cgc Arg	att Ile	gaa Glu	gtt Val 200	gaa Glu	agc Ser	gaa Glu	gaa Glu	gag Glu 205	acc Thr	atc Ile	ggc Gly	624
ggt Gly	cat His 210	ttc Phe	ctg Leu	cac His	ctg Leu	ttg Leu 215	cac	ggc Gly	aaa Lys	cgc Arg	cca Pro 220	agc Ser	gaa Glu	tca Ser	cac	672
atc Ile 225	aaa Lys	gcc Ala	atg Met	cac	gtt Val 230	tca Ser	ctg Leu	att Ile	ctg Leu	tat Tyr 235	gcc Ala	gaa Glu	cac	gag Glu	ttc Phe 240	720
aac Asn	gct Ala	tct Ser	acc Thr	ttt Phe 245	acc Thr	gcc Ala	cgc Arg	gtg Val	atc Ile 250	gcc Ala	ggt Gly	aca Thr	ggc Gly	Ser 255	gat Asp	768
atg Met	tac Tyr	tcc Ser	agc Ser 260	att Ile	acc Thr	gga Gly	gca Ala	atc Ile 265	Gly	gcg	ttg Leu	aaa Lys	ggt Gly 270	Pro	aaa Lys	816
cac His	ggc Gly	ggc G1y 275	Ala	aac Asn	gaa Glu	ggg Gly	Ctt Leu 280	Thr	ata	ttc Phe	aaa Lys	aac Asn 285	Ala	acc Thr	gca Ala	864
atg Met	ccg Pro 290	Thr	aag Lys	ecg	aag Lys	ecg Pro 295	Thr	tcc Ser	gcg	aac Asr	gca Ala 300	Ser	geo Ala	gca Ala	aag Lys	912
	tco Ser	tga	1													921

<400> 38 Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro $1 \\ 5 \\ 10 \\ 15$

Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro $20 \hspace{1cm} 25 \hspace{1cm} 30 \hspace{1cm}$

- Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln . 40 Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro 135 Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe 230 Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys 265 His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys
 - Lys Ser

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<211> 945

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<213> Neisseria meningitidis

<220>

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<222> (1)..(942)

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Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala

260 265 270

gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc 86 Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe 275 280 285

ttt gtc ggc gcc att ctg att att gcc ggt att gtg tct atc aat ggg 912 Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly 290 295 300

ctg tat cga cca ttg ttg aag cga att gaa taa 945 Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu 305 310

<210> 40 <211> 314 <212> PRT

<213> Neisseria meningitidis

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1 10 15

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Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val 35 40 45

Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser 65 70 75 80

Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys

Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr $100 \hspace{1cm} 105 \hspace{1cm} 105 \hspace{1cm} 110 \hspace{1cm}$

Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala 115 120 125

Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile 130 $$135\$

Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala 145 150 155 160

Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala 165 170 175

Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys 180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe 195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu 225 230 240

145

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Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu
                                     250
 Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala
                                 265
 Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe
 Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly
                         295
 Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu
                     310
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<220>
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 gaa tac tac gac gcg cgt gcg gcg tgt gag gac atc aag ccc ggc tct
 Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
 tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc
 Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
 aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt
 Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
 cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg
 Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
 egg gtg gtg tgc cae gat att etg ggg eag ace geg ttg gtg gat ttg
 Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
                                       90
  gea ggt etg ege gat geg att gee gaa aaa gge gge gat eet gee aaa
  Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
                                  105
  gtg aat ccg gtg gtt gca aaa ccc agc ttc atc gtc gac cac tct ctg
  Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu
                              120
  gcc gtt gaa tgc ggc ggc tac gac ccc gat gcc ttc cgc aaa aac cgc
                                                                     432
  Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg
  caa atc qaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg
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Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp

150

155

aca Thr	aaa Lys	acc Thr	gça. Ala	ttt, Phe 165	gaa Glu	aat Asn	gtg Val	Asp	gtg Val 170	att Ile	ccg Pro	gcg Ala	GLY	aac Asn 175	ggc Gly	528
atc Ile	atg Met	cac His	caa Gln 180	atc Ile	aat Asn	cta Leu	gaa Glu	aaa Lys 185	atg Met	tcg Ser	ccc Pro	Val	gtc Val 190	caa Gln	gtc Val	576
aaa Lys	aac Asn	ggc Gly 195	gtg Val	gcg Ala	ttc Phe	ccc Pro	gat Asp 200	acc Thr	tgc Cys	gtc Val	ggc Gly	acg Thr 205	gat Asp	tcg Ser	cac His	624
acg Thr	ccg Pro 210	cac His	gtc Val	gat Asp	gcg Ala	ctg Leu 215	ggc Gly	gtg Val	att Ile	tcc Ser	gtg Val 220	ggc Gly	gtg Val	ggc Gly	gga Gly	672
ttg Leu 225	gaa Glu	gcg Ala	gaa Glu	acc Thr	gtg Val 230	atg Met	ctg Leu	ggt Gly	cgc Arg	gcg Ala 235	tcc Ser	atg Met	atg Met	cgc Arg	ctg Leu 240	720
ccc Pro	gat Asp	att Ile	gtc Val	ggc Gly 245	gtt Val	gag Glu	ctg Leu	aac Asn	ggc Gly 250	aaa Lys	cgg Arg	cag Gln	gcg Ala	ggc Gly 255	att Ile	768
acg Thr	gcg Ala	acg Thr	gat Asp 260	att Ile	gtg Val	ttg Leu	gca Ala	ctg Leu 265	acc Thr	gag Glu	ttt Phe	ctg Leu	cgc Arg 270	aaa Lys	gaa Glu	816
cgc Arg	gtg Val	gtc Val 275	ggg Gly	gcg Ala	ttt Phe	gtc Val	gaa Glu 280	ttc Phe	ttc Phe	ggc Gly	gag Glu	ggc Gly 285	gcg Ala	aga Arg	agc Ser	864
ctg Leu	tct Ser 290	atc Ile	ggc Gly	gac Asp	ege Arg	gcg Ala 295	acc Thr	att Ile	tcc Ser	aac Asn	atg Met 300	acg Thr	ccg Pro	gag Glu	ttc Phe	912
ggc Gly 305	gcg Ala	act Thr	gcc Ala	gcg Ala	atg Met 310	ttc Phe	gct Ala	att Ile	gat Asp	gag Glu 315	GIN	acc Thr	att Ile	gat Asp	tat Tyr 320	960
ttg Leu	aaa Lys	ctg Leu	acc Thr	gga Gly 325	Arg	gac Asp	gac Asp	gcg Ala	cag Gln 330	Val	aaa Lys	ttg Leu	gtg Val	gaa Glu 335	acc Thr	1008
tac Tyr	gcc	aaa Lys	acc Thr 340	· Ala	ggc	tta Leu	tgg Trp	gca Ala 345	Asp	gcc Ala	ttg Leu	aaa Lys	acc Thr 350	MIC	gtt Val	1056
tat Tyr	ccc	ego Arg 355	y Val	ttç Leu	aaa Lys	ttt Phe	gat Asp 360	Leu	ago Ser	ago Ser	gta Val	acg Thr 365	Arg	aat Asr	atg Met	1104
gca Ala	ggc G1 ₅	Pro	g ago Ser	aac Asr	cco	cac His	Ala	cgt Arg	ttt Phe	gcg Ala	acc Thr	: Ala	gat Asp	tto Lei	g gec 1 Ala	1152
ago Sei 385	Lys	gge Gl	tto Y Lei	g gct ı Ala	aaa Lys 390	s Pro	tac Tyr	gaa Glu	ı gaç ı Glu	g cct i Pro 395	se ₂	gac Asp	ggc Gly	caa Glr	a atg n Met 400	1200
Pro	ga As	gg Gl	e geç y Ala	g gto a Va: 40:	l Ile	e ato	gco Ala	geç a Ala	atta Ile	e Thi	c agt	tgo Cys	aco Thi	aa Ası 41	c act n Thr	1248
tc	c aa	000	g cg	c aa	e gt	t gti	ge	e ge	e ge	g ct	e tte	g gcq	g cgo	aa.	e gec	1296

Ser	Asn	Pro	Arg 420.		Val •	Val	Ala	Ala 425	Ala	Leu	Leu	Ala	Arg 430	Asn	Ala	
aac Asn	tgc Cys	ttc Phe 435	ggg Gly	ctg Leu	aaa Lys	cgc Arg	aaa Lys 440	ccg Pro	tgg Trp	gtc Val	aaa Lys	acc Thr 445	tcg Ser	ttt Phe	gcc Ala	1344
Pro	ggt Gly 450	tcg Ser	aaa Lys	gtg Val	gcg Ala	gaa Glu 455	att Ile	tat Tyr	ttg Leu	aaa Lys	gaa Glu 460	gca Ala	ggc Gly	ctg Leu	ctg Leu	1392
ecc Pro 465	gaa Glu	atg Met	gaa Glu	aaa Lys	ctc Leu 470	ggc Gly	ttc Phe	ggt Gly	atc Ile	gtc Val 475	gcc Ala	ttc Phe	gcc Ala	tgc Cys	acc Thr 480	1440
acc Thr	tgc Cys	aac Asn	ggc Gly	atg Met 485	agt Ser	ggc Gly	gcg Ala	ctg Leu	gat Asp 490	ccg Pro	aaa Lys	atc Ile	cag Gln	aaa Lys 495	gaa Glu	1488
atc Ile	atc Ile	gac Asp	cgc Arg 500	gat Asp	ttg Leu	tac Tyr	gcc Ala	acc Thr 505	gcc Ala	gta Val	tta Leu	tca Ser	ggc Gly 510	aac Asn	cgc Arg	1536
aac Asn	ttc Phe	gac Asp 515	ggc Gly	cgt Arg	gtc Val	cat His	ccg Pro 520	tat Tyr	gcg Ala	aaa Lys	cag Gln	gct Ala 525	ttc Phe	ctc Leu	gct Ala	1584
tcg Ser	cct Pro 530	ccg Pro	ttg Leu	gtc Val	gtt Val	gcc Ala 535	tac Tyr	gcg Ala	ctg Leu	gca Ala	ggc Gly 540	agt Ser	atc Ile	cgt Arg	ttc Phe	1632
gat Asp 545	att Ile	gaa Glu	aac Asn	gac Asp	gta Val 550	ctc Leu	ggc Gly	gtt Val	gca Ala	gac Asp 555	ggc Gly	aag Lys	gaa Glu	atc Ile	cgc Arg 560	1680
ctg Leu	aaa Lys	gac Asp	att Ile	tgg Trp 565	cct Pro	gcc Ala	gat Asp	gaa Glu	gaa Glu 570	TTE	gat Asp	gcc Ala	gtc Val	gtt Val 575	gcc Ala	1728
gaa Glu	tat Tyr	gtg Val	aaa Lys 580	Pro	cag Gln	cag Gln	ttc Phe	ege Arg 585	Asp	gtg Val	tat Tyr	gta Val	ccg Pro 590	atg Met	ttc Phe	1776
Asp	Thr	Gly 595	Thr	Ala	Gln	Lys	A1a 600	Pro	Ser	Pro	Leu	605	Asp	110	cgt Arg	1824
Pro	Met 610	Ser	Thr	Tyr	Ile	Arg 615	Arg	Pro	Pro	Tyr	620)	. оту	ALC	ctg Leu	1872
gca Ala 625	. Gl	gaa Glu	. cgc	aca Thr	tta Leu 630	Arg	ggt Gly	ato Met	g egt : Arg	eco Pro 635	ь тег	g gcg ı Ala	att Ile	tto Lev	Pro 640	1920
gac Asp	aac Asr	ato 111e	acc Thr	acc Thr	: Asr	cac His	cto Lev	tcq Sei	g ccq Pro 650	Sei	aat Asi	geq n Ala	att i Ile	tto Let 655	g gee 1 Ala 5	1968
gto Val	agt Sei	gcc Ala	gca Ala 660	a Gly	gaç Glu	tat ı Tyı	tto Lei	g gce 1 Ala 66	а Гуз	a ato	g gg	t tto y Lei	p cct 1 Pro 670) GT	a gaa ı Glu	2016
gad Asi	p Ph	e aad e Asi 67!	n Se:	t tac	gca Ala	a aco	c cad r Hi: 689	s Ar	g gg	c ga y As	e ca p Hi	s Le 68	ı Thi	g gc	c caa a Gln	2064

cgc Arg	gct Ala 690	acc Thr	ttc. Phe	gcc. Ala	aat Asn	ccg Pro 695	aaa Lys	ctg Leu	ttt Phe	aac Asn	gaa Glu 700	atg Met	gtg Val	aaa Lys	aac Asn	2112
gaa Glu 705	gac Asp	ggc Gly	agc Ser	gtg Val	ege Arg 710	caa Gln	ggc Gly	tcg Ser	ttc Phe	gcc Ala 715	cgc Arg	gtc Val	gaa Glu	ccc Pro	gaa Glu 720	2160
			atg Met													2208
			ctc Leu 740													2256
agc Ser	cgc Arg	gac Asp 755	tgg Trp	gct Ala	gca Ala	aaa Lys	ggc Gly 760	gta Val	cgc Arg	ctc Leu	gcc Ala	ggc Gly 765	gta Val	gaa Glu	gcg Ala	2304
			gaa Glu													2352
			ttg Leu													2400
			gac Asp													2448
			gac Asp 820													2496
gtc Val	gaa Glu	gtt Val 835	ccc Pro	gtt Val	acc Thr	tgc Cys	cgc Arg 840	ctc Leu	gat Asp	act Thr	gca Ala	gaa Glu 845	gaa Glu	gta Val	ttg Leu	2544
gta Val	tat Tyr 850	gaa Glu	gcc Ala	ggc Gly	ggc Gly	gtg Val 855	ttg Leu	caa Gln	cgg Arg	ttt Phe	gca Ala 860	cag Gln	gat Asp	ttt Phe	ttg Leu	2592
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Glu	Tyr	Tyr	Asp 20	Ala	Arg	Ala	Ala	Cys 25	Glu	Asp	Ile	Lys	Pro 30	Gly	Ser	
Tyr	Asp	Lys 35	Leu	Pro	Tyr	Thr	Ser 40	Arg	Ile	Leu	Ala	Glu 45	Asn	Leu	Val	
Asn	Arg	Ala	Asp	Lys	Val	Asp	Leu	Pro	Thr	Leu	Gln	Ser	Trp	Leu	Gly	

	50					55					60				
Gln 65	Leu	Ile	Glu	Gly	Lys 70	Gln	Glu	Ile	Asp	Phe 75	Pro	Trp	Tyr	Pro	Ala 80
Arg	Val	Val	Cys	His 85	Asp	Ile	Leu	Gly	Gln 90	Thr	Ala	Leu	Val	Asp 95	Leu
Ala	Gly	Leu	Arg 100	Asp	Ala	Ile	Ala	Glu 105	Lys	Gly	Gly	Asp	Pro 110	Ala	Lys
Val	Asn	Pro 115	Val	Val	Ala	Lys	Pro 120	Ser	Phe	Ile	Val	Asp 125	His	Ser	Leu
Ala	Val 130	Glu	Cys	Gly	Gly	Tyr 135	Asp	Pro	Asp	Ala	Phe 140	Arg	Lys	Asn	Arg
Gln 145	Ile	Glu	Asp	Arg	Arg 150	Asn	Glu	Asp	Arg	Phe 155	His	Phe	Ile	Asn	Trp 160
Thr	Lys	Thr	Ala	Phe 165	Glu	Asn	Val	Asp	Val 170	Ile	Pro	Ala	Gly	Asn 175	Gly
Ile	Met	His	Gln 180	Ile	Asn	Leu	Glu	Lys 185	Met	Ser	Pro	Val	Val 190	Gln	Val
Lys	Asn	Gly 195	Val	Ala	Phe	Pro	Asp 200	Thr	Cys	Val	Gly	Thr 205	Asp	Ser	His
Thr	Pro 210	His	Val	Asp	Ala	Leu 215	Gly	Val	Ile	Ser	Val 220	Gly	Val	Gly	Gly
Leu 225	Glu	Ala	Glu	Thr	Val 230	Met	Leu	Gly	Arg	Ala 235	Ser	Met	Met	Arg	Leu 240
	Asp			245					250					255	
	Ala		260					265					270		
	Val	275					280					285			
	Ser 290					295					300				
305	Ala				310				_	315					320
	Lys			325					330					335	
_	Ala		340		_			345					350		
	Pro	355					360					365			
	Gly 370					375					380				
385	Lys				390					395					400
Pro	Asp	Gly	Ala	Val	Ile	He	Ala	Ala	Ile	Thr	Ser	Cys	Thr	Asn	Thr

405 . 410 . 415

Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala 420 425 430

Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala 435 440 445

Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu 450 460

Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr 465 470 475 480

Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu $485 \hspace{1cm} 490 \hspace{1cm} 495$

Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg $500 \hspace{1.5cm} 505 \hspace{1.5cm} 510$

Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala 515 520 525

Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg 545 550 555 560

Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala 565 570 575

Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe 580 585 590

Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg 595 600 605

Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu 610 615 620

Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro 625 630 640

Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala $645 \hspace{1.5cm} 650 \hspace{1.5cm} 655$

Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Glu 660

Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn 690 695 700

Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu 705 $$ 710 $$ 720

Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg 725 730 735

Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser $740 \hspace{1cm} 745 \hspace{1cm} 750$

Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala

55 760 76

Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly

Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr 785 790 795 800

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr 805 810 815

Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr 820 825 830

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu 835 840 845

Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu 850 855 860

Glu Gly Asn Ala Ala

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gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro

45
46
47

gac ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agt tcg tcc $\,$ 192 Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser $\,$ 50 $\,$ 60 $\,$

acc agc aaa gcc gtg att ttg gac aag tcc gaa cgc acc gat cac gat Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp 65 70 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 28 Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 101 110

atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac ggc ccg 384 Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro 115 120 125

					atc. Ile												432
F	at is 45	gta Val	ccg Pro	atg Met	caa Gln	aac Asn 150	ggc Gly	gca Ala	gtt Val	ttg Leu	gaa Glu 155	aca Thr	ggc Gly	gat Asp	ttt Phe	gag Glu 160	480
					acg Thr 165												528
					ggc Gly												576
					gtg Val												624
					ccg Pro												672
7					ttg Leu												720
					aaa Lys 245												768
					tcc Ser												816
					ccc Pro												864
					gac Asp												912
Ι					gcg Ala												960
					ccc Pro 325												1008
3	ecg Thr	cgt Arg	aaa Lys	gaa Glu 340	gtg Val	cgc Arg	ttc Phe	ggg Gly	cat His 345	cct Pro	tcc Ser	ggc Gly	aca Thr	ttg Leu 350	ege Arg	gtc Val	1056
					gaa Glu												1104
4	gtt Val	atg Met 370	agc Ser	cgc Arg	agc Ser	gca Ala	ege Arg 375	gtg Val	atg Met	atg Met	gaa Glu	ggt Gly 380	tgg Trp	gtc Val	agg Arg	gtg Val	1152
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<213> Neisseria meningitidis

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Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala 105

Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 135

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 210

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu 235

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 265

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly 295

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                325
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
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gea atg ctg ccg gcg tgt tgg gcg cag gcg atg ttg gcc gaa gta atc
Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile
                                  25
age tgc aac aag get teg teg etg eeg eag eet teg geg aga teg geg
Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
ttt aaa tca acc tgc ttc atg ggt gat tct ccg tat ttg gtt cag ata
                                                                   192
Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
gac ttg gtt ttt gcg ccg cag ggc ggt ggc ttc ttt caa gcc gat tat
Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
                      70
                                                                   288
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Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
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 Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu
                                 105
 ege ate ggc cag cag gat aat egg ttt gee gee ggg egg cae etg eae
 Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His
                             120
 ggt tee tge etg aac age gtg gga cag cat tte caa agg ttg ega cag
 Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln
                                             140
                         135
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Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr 65 70 75

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln Ile Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu 105 Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala 155 Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys 185 Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala 200 Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His 230 Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly 245 Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly 280 Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln 295 Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln 310 <210> 47 <211> 648 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(645) <400> 47 atg aga ata gag atc aca cca atc agc gaa tcc gct ttg gtc tgc cga Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg ctg aat gcg cct tcc gaa ctg qqc aaa cag caa aag ttg tqq qcq ttt

Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe

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					gtg Val											192
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					gtg Val											288
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					cat His											384
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					gcc Ala 150											480
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					atc Ile											576
gat Asp	ttg Leu	aat Asn 195	ccg Pro	ccg Pro	acc Thr	ctg Leu	ctg Leu 200	gcg Ala	gcg Ala	ggt Gly	gac Asp	caa Gln 205	gtc Val	cgc Arg	ttt Phe	624
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.04																
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Met			Glu		Thr	Pro	Ile	Ser		Ser	Ala	Leu	Val	Cys	Arg	
Leu		al a	Pro	5 Ser	Glu	Len	G1 17	T.ve	10 Gln	Gln	I.vs	Len	Trn		Phe	
ьeu	ASN	MIA	20		GIU	Leu	GIY	25	GIII	9111	пуъ	10 C	30	21.La	1.16	
Ala	Ala	Ala	Leu	Gly	Gln	His	Asp	Arg	Ile	Glu	Glu	Val	Val	Val	Gly	

Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Val Gly
35 40 45

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Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp
His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr
Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
                                105
Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met
Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
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Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
gac acg gtt gct ttg gcg gcg ggt aat att tta ttg ggc aac gac gaa
Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt
                                                                   192
Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
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qua cqq qat acg ccq ttt tgt ctc acc ggt gcc gtg tat cag gcg gaa
Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
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Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
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ggg Gly	cag Gln	acc Thr	ttg Leu 100	aaa Lys	atg Met	gtg Val	cgt Arg	gcc Ala 105	gtg Val	cag Gln	ggc Gly	atg Met	tac Tyr 110	ggc Gly	tat Tyr	336
gtg Val	tgc Cys	gtg Val 115	gcg Ala	ggc Gly	gga Gly	ttt Phe	gat Asp 120	gtg Val	ccg Pro	gaa Glu	gtg Val	atg Met 125	ggt Gly	tcg Ser	aga Arg	384
agc Ser	acc Thr 130	gac Asp	ctg Leu	aaa Lys	gcc Ala	ggt Gly 135	ttc Phe	ggc Gly	ggc Gly	cat His	cag Gln 140	ggc Gly	aga Arg	atg Met	ctg Leu	432
caa Gln 145	aaa Lys	ggc Gly	gat Asp	tat Tyr	ctc Leu 150	ccc Pro	atc Ile	ggc Gly	aaa Lys	ggt Gly 155	gcg Ala	cag Gln	gaa Glu	ttg Leu	tcc Ser 160	480
aaa Lys	gtc Val	ggc Gly	att Ile	gcc Ala 165	ccg Pro	ata Ile	ccg Pro	ttt Phe	acc Thr 170	gat Asp	acc Thr	atc Ile	cac His	ctt Leu 175	gtt Val	528
cct Pro	tcg Ser	tcg Ser	gaa Glu 180	tat Tyr	gcc Ala	gct Ala	ttc Phe	agt Ser 185	gaa Glu	aaa Lys	ggg Gly	cgt Arg	ctg Leu 190	aat Asn	ctg Leu	576
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ccg Pro	att Ile	atc Ile	ctg Leu	ctg Leu 245	gcc Ala	gat Asp	gcg Ala	caa Gln	acc Thr 250	acc Thr	ggc Gly	ggt Gly	tat Tyr	ccg Pro 255	aaa Lys	768
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gcc Ala	ctg Leu 290	Arg	cgc Arg	aaa Lys	aac Asn	caa Gln 295	Val	tat Tyr	ctg Leu	aac Asn	caa Gln 300	ata Ile	cgg Arg	aga Arg	atc Ile	912
	cat His															930
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Gly Arg Tyr Gly .His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys 235 Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg

Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr 275 280 285

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	cta Leu															144
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	att Ile															240
	gaa Glu															288
tcc Ser	ggc Gly	ttg Leu	ggg Gly 100	cat His	ctt Leu	tta Leu	gtt Val	gag Glu 105	gct Ala	gat Asp	ttg Leu	ccc Pro	atc Ile 110	atc Ile	gct Ala	336
	gcc Ala															384
acc Thr	ttg Leu 130	ccc Pro	ttg Leu	ctg Leu	acc Thr	tgt Cys 135	ttt Phe	ttt Phe	aac Asn	cgg Arg	aaa Lys 140	ata Ile	cat His	aat Asn	gtt Val	432
	gag Glu															480
ctc Leu	gga Gly	tcg Ser	ctt Leu	gcc Ala 165	gcc Ala	gcc Ala	gaa Glu	ttt Phe	ttc Phe 170	tac Tyr	gtc Val	ttt Phe	ttt Phe	acc Thr 175	ctc Leu	528
	caa Gln															576
tca Ser	gta Val	tgc Cys 195	tgc Cys	gtt Val	aca Thr	gaa Glu	agg Arg 200	atg Met	gat Asp	ata Ile	gtg Val	aac Asn 205	act Thr	aaa Lys	ccg Pro	624
aat Asn	act Thr 210	agt Ser	ttg Leu	att Ile	tat Tyr	atg Met 215	ctt Leu	tct Ser	ttc Phe	ctt Leu	agc Ser 220	ggc Gly	tta Leu	ttg Leu	agc Ser	672
ttg Leu 225	ggt Gly	ata Ile	gaa Glu	gte Val	ttg Leu 230	Trp	gta Val	agg Arg	atg Met	ttt Phe 235	Ser	ttc Phe	gca Ala	gca Ala	cag Gln 240	720

too gtg cct cag gca ttt tca ttt act ctt gcc tat ttt ctg acc ggt Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly

O

in.

435

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			aca Thr													1200
gta Val	gca Ala	gtt Val	tcc Ser	cta Leu 405	atg Met	ttc Phe	ggc Gly	atc Ile	ctc Leu 410	atg Met	ttc Phe	cta Leu	ctg Leu	ccg Pro 415	gat Asp	1248

tct Ser	gtc Val	ttt Phe	caa Gln 420	aat Asn	att Ile	gct Ala	gac Asp	cgt Arg 425	ccg Pro	gat Asp	cgg Arg	ctg Leu	att Ile 430	gaa Glu	aac Asn	1296
aaa Lys	cac His	ggc Gly	att Ile	gtt Val	gcg Ala	gtt Val	tac Tyr	cat His	aga Arg	gat Asp	ggt Gly	gat Asp	aag Lys	gtt Val	gtt Val	1344

tat Tyr	Gly	gcg Ala	aat Asn	gta Val	tac Tyr	Asp	ggc Gly	gca Ala	tac Tyr	aat Asn	Thr	gat Asp	gta Val	ttc Phe	aat Asn	1392
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agt	atc	aac	aac	atc	gaa	cgt	gcc	tat	ctg	cta	ccc	tcc	ctg	aag	tct	1440
Ser															Ser	
465					470					475					480	

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GTĀ	TTE	Arg	Arg		FILE	VOL	VCIL	GTA		DCI	1111	011	COL	495		
				485					490					495		

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410

- Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr Val Asp Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met 665 Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
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- Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe

- Arg Ala Ala Ala Ala Val Gln His Ala As
n Ala Ala Asp Gly Val Arg725 , , 730
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- His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu 755 760 765
- Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp 770 780

- Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala $820 \hspace{1.5cm} 825 \hspace{1.5cm} 830$
- Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp 835 840 845
- Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr $850 \\ 850 \\ 860$
- Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly 865 870 875
- Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn 885 890 895
- Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg $900 \hspace{1.5cm} 905 \hspace{1.5cm} 910$
- Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu 915 920 925
- Glý Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala 930 935 940
- Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala $945 \hspace{1.5cm} 950 \hspace{1.5cm} 955 \hspace{1.5cm} 960$
- Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr 965 970 975
- Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg 980 985 990
- Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu 995 1000 1005
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Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
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Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
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Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
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165

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Leu	Ser	Lys	Ile	Pro	Val	Phe	Lys	Gln	Pro	Ala	Pro	Ser	Lys	Ile	Gly	

L)

195 200 Gln Gly Ser Ile Gln Asn Tle Val Leu Ile Met Gly Glu Ser Glu Ser Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile Asn Leu..Glm Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro

Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe 465 470 480

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn $500 \hspace{1.5cm} 505 \hspace{1.5cm} 510 \hspace{1.5cm}$

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln 515

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<213> Neisseria gonorrhoeae

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ttg ctg acg gaa aaa gtg tcg ccc atc atc gca tta atc ttg gtg ccg
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
ctg att ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
ttt tat tog ggc ggc acg aaa tog gtg acg cag att gtg att atg ttt
                                                                   192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc
                                                                   240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg
                                                                   288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
                                                                   336
gca gtg agt gtg ggg acg gtc ttg gtg tcg gtg gtg gca cag ttg gac
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
                                 105
ggg geg ggc geg aeg aeg ttt tta teg gtc gtc eec gec ett ttg eeg
                                                                   384
Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
        115
ctt tac aag egt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
    130
                        135
act too ago gog ggg cta ato aac ctt ttg cog cgg ggc ggg ccg ato
                                                                   480
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
                     150
ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa
                                                                    528
Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
                                                                    576
cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gtg ctg
Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu
             180
tcc ctg ttt ttg ggt gtg cgt gaa aaa agg cgg att gtc cgg gag ttg
                                                                    624
Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
                                                                    672
 ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg gcg cct ttg tcg
Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser
 qua qua qua cau aua ttg qeq eqt eeg aua etg ttt tgg tgg aut gte
Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
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Ile Val Pro Leu Pro 435 <210> 59 <211> 437

Carried Contract

W

C)

job.

(F

C

<212> PRT <213> Neisseria gonorrhoeae

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Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro $20 \hspace{1cm} 25 \hspace{1cm} 30 \hspace{1cm}$

370

Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp 105 Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu 135 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu ... _ 180 Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu 200 Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val 235 Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn 265 Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly 280 Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu 295 Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr 340 Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val

145

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 390 * Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp 410 Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly 425 Ile Val Pro Leu Pro 435 <210> 60 <211> 1155 <212> DNA <213> Neisseria gonorrhoeae <220> <221> CDS <222> (1)..(1152) <400> 60 atq ggc atc cat ctc gac ttc ggc att agt cct aaa acg ttc cga cag Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln 1 act tat..ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn 20 ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val 50 55 240 cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg 70 65 288 tac cgt ttt att aaa toc gtt atc tac gaa cat atg aag aat ggt gcg Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala 85 tog tta gto tat aac cat att aac aac gag cog ttt toa gac cat atc 336 Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile 100 gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga 384 Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly 120 115 tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr 130 cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu

act goo cot gat the cot atg coa the tat atg caa cag act aaa gat

150

Thr Ala	Pro As	Phe 165	Pro	Met	Pro	Leu	Tyr 170	Met	Gln	Gln	Thr	Lys 175	Asp	
act gat Thr Asp	att to Ile Se 18	r Ile	cct Pro	gaa Glu	cat His	atc Ile 185	gat Asp	atg Met	gat Asp	att Ile	atc Ile 190	ctt Leu	gaa Glu	576
gca ggt Ala Gly														624
ccg ctc Pro Leu 210														672
aac ggc Asn Gly 225														720
gaa agt Glu Ser														768
atc aac Ile Asn		r Ala												816
aat tat Asn Tyr	gaa gc Glu Al 275	c ttc a Phe	agt Ser	gaa Glu	gac Asp 280	ttt Phe	ctc Leu	ggc Gly	aaa Lys	gaa Glu 285	cgt Arg	acc Thr	gat Asp	864
acc gct Thr Ala 290	ttt ca Phe Hi	t ctc s Leu	gaa Glu	cag Gln 295	ttc Phe	gcg Ala	aat Asn	ccc Pro	aac Asn 300	gct Ala	act Thr	ccg Pro	ctt Leu	912
tca gac Ser Asp 305														960
gaa áag Glu Lys														1008
ttg ggg Leu Gly	aaa aa Lys Ly 34	s Val	tta Leu	gaa Glu	cac His	atc Ile 345	ggt Gly	aag Lys	aat Asn	gaa Glu	ccg Pro 350	tta Leu	ttg Leu	1056
ttg aaa Leu Lys														1104
agg aag Arg Lys 370	ttg at Leu Il	c tat e Tyr	cag Gln	ttg Leu 375	ata Ile	gag Glu	tta Leu	gat Asp	ttt Phe 380	ctg Leu	gaa Glu	att Ile	ttg Leu	1152
.tga														1155
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ctg ttt ttg ata Leu Phe Leu Ile - 50	ttt ggt aac Phe Gly Asn 55	tat acg cga Tyr Thr Arg	aag aca aca gto Lys Thr Thr Val	gag gga 192 Glu Gly										
caa att tta cct Gln Ile Leu Pro 65														
ggg aca att aca Gly Thr Ile Thr	gcg aaa ttc Ala Lys Phe 85	gtg gaa gat Val Glu Asp 90	gga gaa aag gtt Gly Glu Lys Val	aag gct 288 Lys Ala 95										
ggc gac aag cta Gly Asp Lys Leu 100	ttt gcg ctt Phe Ala Leu	tcg acc tca Ser Thr Ser 105	cgt ttc ggc gca Arg Phe Gly Ala 110	Gly Asp										
agc gtg cag cag Ser Val Gln Gln 115	cag ttg aaa Gln Leu Lys	acg gag gca Thr Glu Ala 120	gtt ttg aag aas Val Leu Lys Lys 125	a acg ttg 384 Thr Leu										
gca gaa cag gaa Ala Glu Gln Glu 130	ctg ggt cgt Leu Gly Arg 135	ctg aag ctg Leu Lys Leu	ata cac ggg aas Ile His Gly Ass 140	gaa acg 432 Glu Thr										
cgc agc ctt aaa Arg Ser Leu Lys 145														
att tcg caa cag Ile Ser Gln Gln	ata gac ggt Ile Asp Gly 165	cag aaa agg Gln Lys Arg 170	cgc att aga ct Arg Ile Arg Le	gcg gaa 528 1 Ala Glu 175										
gaa atg ttg cag Glu Met Leu Gln 180				a Val Pro										
aaa caa gaa atg Lys Gln Glu Met														

aaa ctt gat goc tac'ege ega gaa gaa gte ggg etg ett eag gaa atc $\,$ 67 Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile $\,$ 210 $\,$ 215 $\,$ 220

cgc acg cag aat ctg aca ttg gcc agc ctc ccc caa gcg gca ttga Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala 225 230 235 717

<210> 63

<211> 238 <212> PRT

<213> Neisseria meningitidis

<400> 63

Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala 1 510

Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser 20 25 30

Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile 35 40 45

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly 50 60

Gln Ile_Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr $65~^{\circ}~70~75~80$

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala $85 \hspace{1cm} 90 \hspace{1cm} 95$

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp $100 \hspace{1cm} 105 \hspace{1cm} 110 \hspace{1cm}$

Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu . 115 120 125

Ala Glu Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr 130 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His 145 $$ 150 $$ 155 $$ 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala 195 200 205

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala 225 230 235

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gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$	96												
aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser $$40$$	144												
cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe 50 60	192												
gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile 65 70 80	240												
gca ata ccg aac gtc gaa gtc gga cgg cag gtt gat cct tcc aaa ctg Ala IlePro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu - 85 90 95	288												
ctc ttg agc att gtt ccc gaa cgt acc gag tta tat gcc cat cta tat Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr 100 105 110	336												
ato coc ago agt goa goa ggo ttt ato aag cog aaa gao aag gtt gto Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val , 115 120 125	384												
cta cgt tat cag gca tat ccc tat cag aaa ttc ggg ctt gct tcc ggc Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly 130 135 140	432												
agt gte gta tea gtg gca aaa acg gca ctg ggc aga cag gaa ttg teg Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser 145 $$150$$	480												
gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val 165 170 175	528												
tat etc gtg aaa ata aaa eee gae aaa eea aee aet gea tae ggt Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly 180 185 190	576												
gag gaa aaa ccg ctg caa atc ggc atg acg ctg gaa gca gac atc cta Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu 195 200 205													
cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ccg att tac agt His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser 210 220													
atg tcg ggc agg ttg taa Met Ser Gly Arg Leu	690												

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<213> Neisseria gonorrhoeae
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Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
                                                          95
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
            100
                                105
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
                165
                                    170
                                                     190
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
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Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly

200 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser

215

Met Ser Gly Arg Leu 225

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aat Asn	aat Asn	ttc Phe	ggg Gly 20	ttt Phe	ttg Leu	ege Arg	ctg Leu	ccg Pro 25	ctt Leu	aat Asn	ttt Phe	atg Met	ccg Pro 30	tat Tyr	gaa Glu	96
agc Ser	cat His	gcc Ala 35	gat Asp	tgg Trp	gtt Val	att Ile	acc Thr 40	ggc Gly	gtg Val	cct Pro	tat Tyr	gat Asp 45	atg Met	gcg Ala	gtt Val	144
tca Ser	ggg Gly 50	cgt Arg	tcc Ser	ggc Gly	gcg Ala	egt Arg 55	ttc Phe	ggt Gly	cct Pro	gaa Glu	gcc Ala 60	atc Ile	egg Arg	cgc Arg	gcc Ala	192
tcc Ser 65	gtc Val	aac Asn	ctc Leu	gct Ala	tgg Trp 70	gag Glu	cac His	cgc Arg	agg Arg	ttt Phe 75	ccg Pro	tgg Trp	aca Thr	ttt Phe	gat Asp 80	240
gtg Val	cgc Arg	gaa Glu	ege Arg	ctg Leu 85	aac Asn	att Ile	att Ile	gat Asp	tgc Cys 90	ggc Gly	gac Asp	ttg Leu	gtt Val	ttt Phe 95	tct Ser	288
ttt Phe	ggc Gly	gac Asp	agc Ser 100	agg Arg	gat Asp	ttt Phe	gtc Val	gaa Glu 105	aaa Lys	atg Met	gaa Glu	gcg Ala	cac His 110	gcc Ala	ggc Gly	336
	tta Leu.															384
ttc Phe	att Ile 130	acc Thr	ctc Leu	ccg Pro	ttg Leu	ttg Leu 135	cgc Arg	gcc Ala	cac His	gcc Ala	ege Arg 140	tat Tyr	ttc Phe	ggc Gly	aaa Lys	432
ctc Leu 145	gca Ala	ctg Leu	att Ile	cat His	ttt Phe 150	gac Asp	gcg Ala	cac His	acc Thr	gac Asp 155	acc Thr	tac Tyr	gac Asp	aac Asn	ggc Gly 160	480
agc Ser	gaa Glu	tac Tyr	gac Asp	cac His 165	ggc Gly	acg Thr	atg Met	ttt Phe	tat Tyr 170	acc Thr	gcc Ala	ecc Pro	aag Lys	gaa Glu 175	ggc Gly	528
ctc Leu	atc Ile	gac Asp	ccg Pro 180	tcc Ser	cgt Arg	tcc Ser	gta Val	caa Gln 185	atc Ile	ggc	ata Ile	ege Arg	acc Thr 190	gaa Glu	cac His	576
agt Ser	aaa Lys	aaa Lys 195	ttg Leu	cct Pro	ttt Phe	act Thr	gtg Val 200	Leu	tcc Ser	gcc Ala	ccc Pro	aaa Lys 205	gtc Val	aat Asn	gaa Glu	624
gac Asp	agt Ser 210	gtt Val	gaa Glu	gag Glu	acc Thr	gtc Val 215	cgt Arg	aaa Lys	atc Ile	aaa Lys	gaa Glu 220	acc Thr	gtc Val	ggc Gly	aat Asn	672
atg Met 225	ccc Pro	gtt Val	tac Tyr	ctg Leu	act Thr 230	ttc Phe	gac Asp	ata Ile	gac Asp	tgt Cys 235	Leu	gac Asp	ccg Pro	tcg Ser	ttc Phe 240	720
gcc Ala	ccc Pro	ggg Gly	acc Thr	ggt Gly 245	Thr	ccc	gta Val	tgc Cys	ggc Gly 250	Gly	ttg Leu	agc Ser	agc Ser	gac Asp 255	Arg	768
gca Ala	tta Leu	aaa Lys	atc Ile	cta Leu	cgt Arg	ggg Gly	ctg Leu	acg Thr	gat Asp	ctc Leu	gac Asp	atc	gtc Val	ggt	atg Met	816

260 265 gat gtt gta gaa gtť gcc ccc tct tac gac caa tcc gac att acc gct Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala 280 912 ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala 295 300 924 aaa aag gac tga Lys Lys Asp 305 <210> 67 <211> 307 <212> PRT <213> Neisseria gonorrhoeae <400> 67 Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His 120 Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys 135 Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly 150 Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly 165 Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His 185 180 Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu 200 195

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe 225 230 235 235

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Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
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Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
Lys Lys Asp
305
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Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
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aaa too tat ttt too aaa tat ato ota ooc gtt toa ott ttt aco ttg
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Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
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Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
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Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
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ott occ cat gta toc gec aat goo ago tac cag ogo cag eeg cea tog
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Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 2.65 Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 280 Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 300 295 Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 315 Ser Ser Ala Glm Asm Asm Asp Tyr His Tyr Arg Gly Lys Gly Met Ser Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 395 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 430 Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu 440 Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val 460 Phe Ala Glu 465 <210> 70 <211> 696 <212> DNA <213> Neisseria gonorrhoeae <220> <221> CDS <222> (1)..(693) <400> 70 atg aaa caa too goo oga ata aaa aat atg gat cag aca tta aaa aat Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn aca ttg ggc att tgc gcg ctt tta gcc ttt tgt ttt ggc gcg gcc atc 96 Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile 25 20

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Thr	Let	ı Gly	/ Ile)				23	5				3(,	ılle	
	_		-				. m	- 01-	. m	- 01.	· myy	- 70	Tro	· Car	- Ala	

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala

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	tat	gto Val	g aas L Lys	a ccq s Pro 580	Glr	g caa	n ttt	cgo Aro	g gad g Asp 58!	o Val	tat L Tyr	ato	e cag	g ato Met 590	: Phe	e gac e Asp	1776

GENERAL COLUCT

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Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu 140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile

Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys

170

185 Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr 200

Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 215

Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 235 230

Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr 245

Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg 265 260

Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu 280

- Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 290 300
- Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu 305 310 315 320
- Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr \$325\$
- Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr 340 345 350
- Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala 355 360 365
- Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly $370 \ \ 375 \ \ 380$
- Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro 385 390 395
- Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn 420 425 430
- Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro .435 440 445
- Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro $_{\rm 450}$
- Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr 465 470 470 475
- Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile , 485 490 495
- Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn 500 Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser
- 515 520 525
- Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp 530 540
- Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu 545 550 555 560
- Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu 565 570
- Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro $595 \hspace{0.5cm} 600 \hspace{0.5cm} 605 \hspace{0.5cm}$
- Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 610 620
- Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp 625 630 635 640

Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp 665 Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg 680 Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu 695 Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys 730 Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser 745 Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu 795 785 ---Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val 835 Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu Gly Asn Ala Ala 865 <210> 74 <211> 1170 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(1167) <400> 74 atg ceg caa att aaa att eee gee gtt tae tae egt gge ggt aca tea 48 Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser 96

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gat Asp	ccc Pro 50	tac Tyr	ggc Gly	aag Lys	cag Gln	ata Ile 55	gac Asp	ggt Gly	ttg Leu	ggc Gly	aac Asn 60	gcc Ala	agc Ser	tcg Ser	tcc Ser	192
acc Thr 65	agc Ser	aag Lys	geg Ala	gtg Val	att Ile 70	ttg Leu	gac Asp	aag Lys	tcc Ser	gaa Glu 75	ege Arg	gcc Ala	gat Asp	cac His	gat Asp 80	240
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tgg Trp	agt Ser	ggc Gly	aac Asn 100	tgc Cys	ggc Gly	aac Asn	ctc Leu	acc Thr 105	gcc Ala	gcc Ala	gtg Val	ggc Gly	gca Ala 110	ttt Phe	gcc Ala	336
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tgc Cys	aca Thr 130	gtc Val	aaa Lys	atc Ile	tgg Trp	cag Gln 135	aaa Lys	aac Asn	atc Ile	ggc Gly	aaa Lys 140	acc Thr	att Ile	att Ile	gcc Ala	432
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gat Asp	cca Pro	gcc Ala	gac Asp 180	ggc Gly	gaa Glu	ggc Gly	agt Ser	atg Met 185	ttc Phe	cca Pro	acc Thr	ggc Gly	aat Asn 190	ttg Leu	gtc Val	576
gat Asp	a a a	att Ile 195	Asp	gtg Val	ccg Pro	aat Asn	ata Ile 200	Gly	cgt Arg	ttg Leu	aaa Lys	gcc Ala 205	Thr	ctc	atc Ile	624
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acg Thr 225	. GJ?	aaa Lys	gag Glu	ttg Leu	caa Gln 230	. Asp	gac	atc Ile	aac	aac Asr 235	. Asp	gcc Ala	gca Ala	get Ala	ttg Leu 240	720
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gco Ala	e tto	gto vai	L Ala	g cco	e geo Ala	gco Ala	gat Asp 280	Tyr	acc Thr	gco Ala	tco a Ser	agt Ser 285	: Gl:	e aaa y Lys	acc Thr	864
gto Val	g aa L Ası	t go	e geo a Ala	e gad a Asj	e ato	c gat e Asp	tte	g cto	g gta ı Val	a cge L Are	g gco	c cto	g age	c ato	g ggc : Gly	912

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Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val 185 Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile 200 Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 215 Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 265 Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 280 Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly 295 Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr 315 305 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly 325 330 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val 345 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val 375 Pro Glu Asp Cys Phe <210> 76 <211> 2094 <212> DNA <213> Neisseria gonorrhoeae <220> <221> CDS <222> (1)..(2091) atg aat teg acc gca agt aaa acc etg aaa gga ttg teg etg gtg ttt 48 Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144

Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile 40

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cgc Arg 65	att Ile	gct Ala	gac Asp	cgt Arg	ttt Phe 70	cct Pro	tca Ser	agt Ser	atc Ile	atc Ile 75	ccc Pro	ctg Leu	ttt Phe	tgc Cys	atc Ile 80	240
gct Ala	gaa Glu	gta Val	tcc Ser	atc Ile 85	ggt Gly	ctg Leu	ttc Phe	ggt Gly	ttg Leu 90	gta Val	agc Ser	aag Lys	ggt Gly	ctg Leu 95	att Ile	288
tcc Ser	ggc Gly	ttg Leu	ggg Gly 100	cat His	ctt Leu	tta Leu	gtt Val	gag Glu 105	gct Ala	gat Asp	ttg Leu	ccc Pro	atc Ile 110	atc Ile	gct Ala	336
gct Ala	gcc Ala	aat Asn 115	ttc Phe	ctc Leu	tta Leu	ttg Leu	ctg Leu 120	ctt Leu	cct Pro	acc Thr	ttt Phe	atg Met 125	atg Met	ggc Gly	gcg Ala	~384
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gat Asj	t ttt p Phe 290	e Lev	g att	t tto	g ggt u Gl	gct / Ala 295	a Ala	g tgq a Trp	tto Lev	g tto ı Lev	g acc i Th: 30	r GT7	ttt Phe	tce Se:	c ggt r Gly	912
tt. Ph	c gte e Val	c ca	c ca	c gc	c ggt a Gl	att	tt:	c att	t acc	c cto	g tc u Se	t gco r Ala	gto Val	e gt L Va	c agg l Arg	960

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atg Met	ttt Phe	aat Asn 595	acc Thr	acg Thr	cac His	agc Ser	ccg Pro 600	cat His	gct Ala	ttt Phe	gct Ala	acc Thr 605	gcc Ala	gta Val	cac His	1824
agt Ser	att Ile 610	ccc Pro	tat Tyr	gca Ala	tac Tyr	cgc Arg 615	tac Tyr	Gly ggg	cat His	atg Met	gta Val 620	gtc Val	ggc Gly	tcg Ser	gca Ala	1872
acc Thr 625	ccg Pro	gta Val	gtt Val	ttc Phe	cct Pro 630	aat Asn	aaa Lys	gaa Glu	ctg Leu	ctc Leu 635	aag Lys	caa Gln	cgc Arg	ctt Leu	tcc Ser 640	1920
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acg Thr	gaa Glu	cct Pro 675	tcg Ser	gct Ala	Gly ggg	gcg Ala	gaa Glu 680	gtc Val	att Ile	act Thr	gac Asp	gat Asp 685	aat Asn	atg Met	att Ile	2064
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 - 450 455 460

 Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 465 470 475

 Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 505 500 Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala 520 Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg 535 530 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala 565 Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val 585 Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser 635 625 630 Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr 645 Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met 665 Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile 685 680 Val Glu Tyr Lys Tyr Gly Arg Gly Ile 690 695 <210> 78 <211> 39 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: primer <400> 78 39 getetagace accatgtetg aagaaaaatt gaaaatgag <210> 79 <211> 32 <212> DNA <213> Artificial Sequence

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- (71) Déposants (pour tous les Etats désignés souf US): PASTEUR MERIEUX SERUMS ET VACCINS [FR/FR]: 58, avecus Leclerc, F-69007 Lyon (FR). INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (IN-SERM) [FR/FR]: 10], rue de Toibies, F-75013 Paris (FR).
- (72) Inventeurs; et (75 Inventeurs) depoints (US seulement): AUJAME. Luc [FR/FR]: 477, chemin du Puits, F-69210 Fleurieux-aur-L'Arbresle (FR). BOUOCHARDOM, Annabelle [FR/FR]: 7, ne Nicolai, F-69007 Lyon (FR). RENAULD-MONGENIE, Geneviève [FR/FR]: 24, ne des Framboisiers, F-6960 Chaponost (FR/FR); C4, ne des Framboisiers, F-6960 Chaponost (FR/FR), ROKBI, Bachra [FR/FR]; 254, ne Vendome, F-69003 Lyon (FR), NASSIF, Xavier [FR/FR]; 3, auer Charles Laurent, F-75015 Paris (FR). TINSLEY, Colin [FR/FR]; 16, square Jean Thébaud, F-75015 Paris (FR). PERRIN, Agnès [FR/FR]; 33 bis, ne

du Docteur Roux, F-75015 Paris (FR).

- (74) Mandataires: MONCHENY, Michel etc.; Cabinet Lavoix, 2, place d'Estienne d'Orves, F-75441 Paris Cedex 09 (FR).
- (81) Etats désignés: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HB, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MN, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, brevet ARPIO (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), brevet eurasien (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), brevet eurapéen (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, brevet OAPI (GF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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- (57) Abstract

The invention concerns nucleic acids coding for polypeptides specific of the Neisseria genus pathogenic strains, the corresponding polypeptides, and their diagnostic and therapeutic applications.

(57) Abrégé

Cette invention concerne des acides nucléiques codant pour les polypeptides spécifiques des souches pathogènes du genre Neisseria, les polypeptides correspondants, et leurs applications diagnostiques et thérapeutiques.

PCT/FR99/02643

Nucleic acids and polypeptides specific for pathogenic strains of the Neisseria genus.

The present invention relates to nucleic acids encoding polypeptides specific for pathogenic strains of the Neisseria genus, in particular which are useful for preventing or treating a Neisseria meningitidis infection.

In general, meningitis is either of viral origin or of bacterial origin. The bacteria mainly responsible are: type b Haemophilus Neisseria meningitidis and Streptococcus pneumoniae. The Neisseria meningitidis species is subdivided into serogroups according to the nature of the capsular polysaccharides. Although about a dozen serogroups exist, 90% of meningitis cases can be attributed to three serogroups: A, B and C.

Effective vaccines based on polysaccharides exist for preventing meningitis caused by Neisseria meningitidis serogroups A and C. These polysaccharides, unmodified, are only immunogenic, or not at all, in children under the age of two, and do not induce any immune memory. However, these drawbacks can be overcome by conjugating these polysaccharides to a carrier protein.

On the other hand, the polysaccharide of Neisseria meningitidis serogroup B is non-immunogenic, or relatively non-immunogenic in humans, whether or not it is in a conjugated form. Thus, it appears to be highly desirable to seek a vaccine against meningitis in particular caused by Neisseria meningitidis, Neisseria meningitidis serogroup B, other than a vaccine based on polysaccharide.

To this end, various proteins of the external membrane of N. meningitidis have already been proposed, as the membrane-bound receptor transferrin (WO 90/12591 and WO 93/06861).

Neisseria meningitidis is genetically very close to Neisseria gonorrhoeae and Neisseria lactamica.

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N. gonorrhoeae is especially responsible for infections located in the urogenital tract. It colonizes the genital mucous membrane, crosses the epithelium and then invades the sub-epithelium, where it multiplies and is responsible for a severe inflammatory reaction. On the other hand, N. lactamica is considered to be a nonpathogenic species.

Sequences present in N. gonorrhoeae and N. meningitidis, but absent from N. lactamica, have been disclosed in patent application WO 98/02547, but this prior patent application does not locate or identify the coding sequences.

The authors of the present invention have now managed to identify some of these genes by searching, in the meningococcal genome, for the open reading frames specific for pathogenic strains of the Neisseria genus, using the following strategy:

Some of the sequences disclosed in patent application WO 98/02547 (referred to, in said prior application, as SEQ ID Nos 66, 67, 69, 70, 72 to 96, 98 and 99) were positioned on the sequence of the genome of the N. meningitidis serogroup B strain (ATCC 13090), available from the Pathoseq® bank of Incyte Pharmaceuticals, and also on the sequence of the genome of the Neisseria meningitidis strain Z2491 (Sanger Centre). This made it possible to identify, in the N. meningitidis genome which has 2.3 mega bases, 19 contigs representing 220 000 base pairs.

The authors of the present invention then
analysed, for each of the 19 contigs, the presence of
open reading frames (ORFs) containing at least
100 amino acids (and, by definition, bordered by an
initiation codon and a stop codon), using the Gene
Jockey II sequence processor® program (Biosoft). This
analysis made it possible to select approximately 400
candidate ORFs.

The sequences of each of these ORFs were then analysed using the Codon Use® program (Conrad Halling), which takes into account the codon use frequency in

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N. meningitidis. Only the ORFs with sequences having a maximum frequency of use of these codons were selected. At the end of this analysis, 197 candidate ORFs were selected.

The ORFs selected using this double analysis were subjected to a homology search through all of the available banks, using the BLASTX® program, from the access to the Pathoseq® bank of Incyte Pharmaceuticals. This homology search made it possible to exclude the ORFs encoding, a priori, cytoplasmic or periplasmic proteins, in particular metabolism proteins. The ORFs were also subjected to analysis of possible protein motifs, using the DNA Star Protean® program (Lasergene software).

The authors of the present invention then investigated whether the ORFs selected at the end of the previous step (118 in number) were effectively absent from N. lactamica, as predicted by the application of the prior art WO 98/02547.

To this end, a PCR amplification was carried out. This amplification proved to be ineffective for 78 of the 118 ORFs tested. Only the ORFs for which the amplification in N. lactamica was negative (sequences named "lactamica") were selected. In order to verify that these negative results were not "false negatives", the lactamica sequences selected were subjected to a control by dot blot. At the end of this step, only 23 ORFs were confirmed N. meningitidis*/N. lactamica.

Finally, these 23 ORFs were repositioned in their entirety on the N. meningitidis ATCC13090 genome. 30 This made it possible to demonstrate that three ORFs previously eliminated on the basis of their putative protein function appeared to be located close to, or of framed by, some N. meningitidis '/N. lactamica ORFs. These three ORFs (SEQ ID Nos 29, 35 and 37) were reintroduced into the was proven that they were also it and N. meningitidis*/N. lactamica.

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authors of the present invention then attempted to discover whether the ORFs identified using the genome of the N. meningitidis serogroup B strain ATCC 13090 were also present in the genomes of N. meningitidis serogroup A Z2491 (Sanger Centre) and of N. gonorrhoeae FA1090 (Advanced Centre of Genome Technology, Oklahoma University). Then, they compared the sequences derived from these various genomes, with multiple alignment (Clustal, Infobiogen). This made it possible to redefine, for some of the ORFs, the most initiation codon probable position of the translation stop codon. The sequences of the open reading frames derived from the strain ATCC13090 are given in the SEQ ID Nos 1-51 (odd numbers) and the amino acid sequences which are deduced therefrom are given in the SEQ ID Nos 2-52 (even numbers).

A subject of the present invention is, therefore, a nucleic acid in isolated form encoding a polypeptide, or an antigenic fragment thereof, excluding the nucleic acids disclosed in SEQ ID Nos 70, 73, 74, 77, 80, 81, 87, 88, 89, 94, 95 and 98 of application WO 98/02547 (sequences attached to the present description and numbered SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A so as to distinguish them from the sequences of the invention); said polypeptide having an amino acid sequence which is identical or homologous to a sequence selected from those of group II; group II consisting of the sequences shown in SEQ ID Nos 2-52 (even numbers) and the sequence SEQ ID No. 53.

Preferably, said nucleic acid can have a nucleotide sequence selected from those of group I, group I consisting of the sequences shown in SEQ ID Nos 1-51 (odd numbers).

The term "nucleic acid" includes and means equally ORF, gene, polynucleotide, DNA and RNA. The term "nucleic acid in isolated form" means a nucleic acid separated from the biological environment in Which it is found under natural conditions. For example, a

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DNA molecule exists under natural conditions when it is integrated into a genome or when it forms part of a library of genes. In that case, it cannot be in isolated form. On the other hand, the same molecule separated from the genome by cloning (for example subsequent to a PCR amplification) should be considered as being in isolated form. Typically, a DNA molecule in isolated form does not contain the coding regions which are contiguous with it in 5' and 3' in the genome from which it is derived. The nucleic acids in isolated form can be integrated into vectors (for example plasmids, or viral or bacterial vectors) without, even so, abandoning their characteristic of being separated from their natural environment.

The authors of the present invention have more particularly found that the ORFs which, when they are derived from the strain ATCC 13090, are characterized by the sequences as shown in SEQ ID Nos 19, 27, 39, 45, 47 and 49 are specific for Neisseria meningitidis insofar as it has not been possible to demonstrate identical or homologous sequences in the N. gonorrhoeae genome. They have also found that the ORF characterized by the strain sequence as shown in SEQ ID No. 39 is specific for Neisseria meningitidis serogroup B.

A subject of the invention is also a polypeptide in isolated form, or a fragment thereof; said polypeptide having an amino acid sequence identical or homologous to a sequence selected from those of group II.

The amino acids framed in the sequence SEQ ID No. 8 correspond to the signal sequence, and the amino acid in bold represents the first amino acid of the mature form. The amino acid sequence of the mature protein form is represented in SEQ ID No. 53.

In the context of the present invention, the terms "polypeptide" and "protein" are equivalent and mutually interchangeable. They refer to any amino acid chain, whatever its length and its post-translational

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modifications (for example phosphorylation or qlycosylation).

The expression "antigenic fragments of polypeptides specific for pathogenic strains of the 5 Neisseria genus" is intended to mean the polypeptides derived from the polypeptides of the invention as defined above, through deletions of portions of said polypeptides without destroying the antigenicity (for example, without notable loss of the antigenic polypeptides. The 10 activity) of said specific antiqueicity can be determined using various methods known to those skilled in the art, as explained later.

These fragments are preferably at least 12 amino acids long, more preferably at least 20 amino acids long, preferentially 50 amino acids long, more preferably still 75 amino acids long, preferentially 100 amino acids long.

These fragments can be used to reveal epitopes which may be masked in the parent polypeptides. They are also advantageous for inducing a T-lymphocyte-dependent protective immune response. The deletions can, in fact, make it possible to eliminate immunodominant regions which are highly variable between various strains.

Such fragments can be obtained using standard techniques known to those skilled in the art (for example, Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc, 1994), for example by PCR, RT-PCR or treatment with restriction enzymes for the cloned DNA molecules, or by the method of Kunkel et al. (Proc. Natl. Acad. Sci. USA (1985) 82:448).

The expression "homologous amino acid sequence" is intended to mean a sequence which differs from one of the sequences of group II by substitution, deletion and/or insertion of one or more amino acids, at positions such that these modifications do not destroy the specific antigenicity of the polypeptide in question.

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Said substitutions are preferably conservative substitutions, i.e. substitutions of amino acids of the same class, such as substitutions of amino acids with uncharged side chains (for instance asparagine, glutamine, serine, threonine and tyrosine), of amino acids with basic side chains (for instance lysine, arginine and histidine), of amino acids with acid side chains (for instance aspartic acid and glutamic acid) or of amino acids with apolar side chains (for instance glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan and cysteine).

Advantageously, a homologous amino acid sequence has at least a 75% degree of homology (i.e. of identity) with one of the sequences of group II; preferably this degree of homology is at least 80%, most preferably at least 90%. The homologous amino acid sequences include, in particular, the sequences which are substantially identical to one of the sequences of group II. The expression "substantially identical sequence" means a sequence which has at least a 90%, advantageously at least a 95%, preferably at least a 97%, and most preferably at least a 99%, degree of homology (i.e. of identity) with one of the sequences of group II. In addition, it may differ from the reference sequence only through mainly conservative substitutions.

The degree of homology (also named degree of identity) is generally determined using a sequence analysis program (for example, Sequence Analysis 30 Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Centre, 1710 University Avenue, Madison, WI 53705). Similar amino acid sequences are aligned so as to obtain the maximum degree of homology (i.e. identity). To this end, it may 35 be necessary to artificially introduce gaps into the sequence. Once optimal alignment has been produced, the degree of homology (i.e. identity) is established by recording all the positions for which the amino acids

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of the two sequences compared are identical, with respect to the total number of positions.

The expression "homologous nucleotide sequences" is intended to mean sequences which differ 5 from the sequences of group I by substitution of one or more nucleotides, or by deletion and/or insertion of one or more codons, at positions such that these sequences (i) still encode polypeptides having the sequences of group II, due to the effect of the 0 degeneracy of the genetic code; or (ii) encode polypeptides having homologous sequences as defined above.

Advantageously, a homologous nucleotide sequence has at least a 60% degree of homology with one of the sequences of group I; preferably this degree of homology is at least 80%, most preferably at least 90%.

Typically, a homologous nucleotide sequence hybridizes specifically to the sequences complementary to the sequences of group I, under stringent conditions. The temperature at which the hybridization assay is carried out constitutes an important factor which influences the stringency. Conventionally, this temperature, termed hybridization temperature (Th), is selected from 5 to 40°C, preferably from 20 to 25°C, below the temperature at which 50% of the paired strands separate (Tm). In general, it is considered that conditions of high stringency are satisfied when Th is lower than Tm by 5 to 25°C approximately, for example by 5 to 10°C or, most commonly, by 20 to 25°C approximately. Moderate stringency is established when Th is lower than Tm by 30 to 40°C.

For sequences comprising more than 30 bases, the temperature Tm is defined by the equation: $Tm = 81.5 + 0.41(\$G+C) + 16.6Log(cation concentration) - 0.63(\$formamide) - (600/number of bases). Thus, ionic strength has a major impact on the value of Tm. The temperature Tm increases by <math>16.6^{\circ}C$ every time the monovalent cation concentration increases by a factor of 10. The addition of formamide into the hybridization

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buffer causes, on the other hand, the value of Tm to decrease. (For a complete reference, see Sambrook et al., Molecular Cloning, A laboratory manual, Cold Spring Harbor Laboratory Press, 1989, pages 9.54-9.62).

Conventionally, hybridization experiments are carried out at a temperature of 60 to 60°C, for example at 65°C. At this temperature, stringent hybridization conditions can, for example, be implemented in 6xSC, advantageously in 2xSSC or 1xSSC, preferably in 0.5xSSC, 0.3xSSC or 0.1xSSC (in the absence of formamide). A solution of 1xSSC contains 0.15 M of NaCl and 0.015 M of sodium citrate.

For this reason, in other words, a subject of the invention is a polynucleotide in isolated form, which is capable of hybridizing, under stringent conditions, with a DNA molecule having one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers) or the sequences complementary thereto.

specific class of homologous sequences consists of those encountered naturally by virtue of 2.0 the extremely common phenomenon of allelic variation. A species, for example N. meningitidis or bacterial N. gonorrhoeae, consists of a large variety of strains which differ from one another through minor variations, termed allelic variations. Thus, a polypeptide which is 25 present in various strains and which, of course, performs the same biological function in each of them, can have an amino acid sequence which is not identical from one strain to the other. In other words, the sequences derived from the allelic variation are purely 30 sequences equivalent or alternative to those of group II. The class of sequences which are allelic variants of one of the sequences of group II consists of the sequences of the polypeptide as found in a pathogenic species of the Neisseria genus (for example, 35 N. meningitidis or N. gonorrhoeae) other N. meningitidis strain ATCC 13090. The biological function which is associated with the allelic variant sequences is the same as that which is associated with 1.0

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the reference sequence. The differences (substitution, deletion or addition of one or more amino acids) which they exhibit between one another (including the reference sequence) do not modify the biological function of the polypeptide. The term "biological function" is intended to mean the function exercised by the polypeptide in the cells which produce it naturally.

The allelic variation is also expressed in the coding sequences. A polynucleotide, encoding a polypeptide, having a sequence which is an allelic variant of one of the sequences of group I can be easily cloned by amplifying the genomic DNA of the strains of pathogenic species of the Neisseria genus, for example by PCR (polymerase chain reaction), using synthetic oligonucleotide primers capable hybridizing to the 5' and 3' ends of the coding region. The sequences of such primers can easily be established by those skilled in the art using the nucleotide sequences given in SEQ ID Nos 1-51 (odd numbers). The primers generally have from 10 to 40 nucleotides, preferably from 15 to 25 nucleotides.

For this reason, in other words, a subject of the invention is a DNA molecule in isolated form which can be amplified and/or cloned by PCR from the genome of a pathogenic Neisseria strain, using a pair of 5' and 3' PCR primers; the sequences of these primers being established using one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers). An example 30 is given, for each pair of primers, in Example I.1 hereinafter.

A subject of the present invention is more particularly the allelic variants having the nucleotide sequences SEQ ID Nos 54 to 76 (even numbers) and the products encoded by these nucleotide sequences, having the amino acid sequences SEQ ID Nos 55 to 77 (odd numbers).

The polypeptides of the invention can be fused to other polypeptides, for example by translation of a

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hybrid gene. Vectors for expressing fusion polypeptides are commercially available, such as the vectors pMal-c2 or pMal-p2 from New England Biolabs, in which the protein to which the polypeptides of the invention can be fused is a maltose-binding protein, the glutathione-S-transferase system from Pharmacia or the His-Tag system from Novagen. Such systems are in particular useful for purifying the polypeptides of the invention. The polypeptides of the invention can be fused to polypeptides having adjuvant activity, such as for example the B subunit of cholera toxin or the B subunit of the E. coli heat-sensitive toxin.

The nucleic acids of the present invention can be used (i) in a process for producing the polypeptides encoded by said nucleic acids, in a recombinant host (ii) for the construction of vaccination system, vectors, such as poxviruses, intended to be used in methods and compositions for preventing and/or for infection with pathogenic Neisseria an treating in particular with Neisseria meningitidis, strains, (iii) as a vaccination agent in a naked form or in combination with a vehicle which promotes transfer to the target cells and, (iv) in the construction of attenuated Neisseria strains which can overexpress a nucleic acid of the invention, or express it in a nontoxic, mutated form.

The present invention also provides (i) expression cassette containing a polynucleotide of the invention placed under the control of elements allowing its expression, in particular under the control of a suitable promoter; (ii) an expression vector containing host cassette; (iii) а said expression (prokaryotic or eukaryotic) transformed with an expression cassette and/or an expression vector as defined above, and (iv) a method for obtaining a polypeptide encoded by said polynucleotide of the invention, comprising culturing said transformed cell under conditions allowing the expression

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polynucleotide of the invention, and recovering the polypeptide from the cell culture.

Among the eukaryotic hosts which can be used, mention may be made in particular of yeast cells (for example Saccharomyces cerevisiae or Pichia Pastoris), mammalian cells (for example COS1, NIH3T3 or JEG3) arthropod cells (for example Spodoptera frugiperda (SF9)) and plant cells. Among the prokaryotic hosts which can be used, mention may be made in particular of E. coli.

The choice of the expression cassette depends system chosen, and also characteristics desired for the expressed polypeptide. In general, expression cassettes include a promoter which is functional in the host system selected and which can be constitutive or inducible; a ribosomebinding site; an initiation codon (ATG); if necessary, a region encoding a signal peptide; a nucleotide sequence of the invention; a stop codon; and, optionally, a 3' terminal region (translation and/or transcription terminator). The open reading frame (ORF) consisting of the nucleotide sequence of the invention, alone or associated with the region encoding the signal peptide, is placed under the control of the promoter such that translation and transcription take place in the host system. The promoters and regions encoding the signal peptides are known to those skilled in the art. Among them, mention may be made in particular of the arabinose-inducible promoter (araB promoter) of Salmonella typhimurium, which is functional in Gram bacteria such as E. coli (US 5,028,530 and Cagnon et al., Protein Engineering (1991) 4(7): 843), the promoter of the T7 bacteriophage gene encoding RNA polymerase (US 4,952,496), and the OspA and RlpB signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The polypeptide expressed can be recovered in a practically purified form from the cell extract or from the supernatant, after centrifuging the recombinant cell culture. The recombinant polypeptide can, in

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particular, be purified using methods of affinity purification with the aid of antibodies, or using any other method known to those skilled in the art, for instance by genetic fusion with a small binding domain.

The nucleic acids of the invention can also be used in the field of vaccination, either by using a viral or bacterial host as a vehicle for releasing the DNA, or by administering the nucleic acid of interest in a free form.

A subject of the present invention is also (i) a vaccination vector containing a nucleic acid of the invention, placed under the control of elements allowing its expression; (ii) a pharmaceutical therapeutically composition containing a prophylactically effective amount of said vaccination vector; (iii) a method for inducing an immune response against Neisseria in a vertebrate, in particular a mammal, preferably a human, said method comprising the administration to said vertebrate of an immunologically effective amount of said vaccination vector so as to cause an immune response, in particular a protective or therapeutic response to Neisseria meningitidis; and (iv) a method for preventing and/or treating infection with pathogenic Neisseria strains, particular with Neisseria meningitidis, which comprises the administration of a prophylactic or therapeutic amount of said vaccination vector of the invention to an individual requiring such a treatment.

In combination with the polypeptides of the invention, the vaccination vector as defined above can also comprise nucleotide sequences the expression of which allows the immune response to be stimulated, such as the sequences encoding cytokines.

Said vaccination vector of the invention can be
administered via any route which is conventional in the
field of vaccination, in particular via the parenteral
route (for example subcutaneous, intradermal,
intramuscular, intravenous or intraperitoneal route).
The dose depends on many parameters which are known to

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those skilled in the art, such as the vector itself, the route of administration, or the weight, age or sex of the animal or of the human to be vaccinated.

A subject of the present invention is also (i) pharmaceutical composition containing therapeutically or prophylactically effective amount of a polynucleotide of the invention; (ii) a method for response against pathogenic inducing an immune Neisseria strains, in particular Neisseria meningitidis in a vertebrate, by administering to said vertebrate an immunologically effective amount of said polynucleotide so as to cause an immune response, in particular a protective immune response against pathogenic Neisseria strains, especially Neisseria meningitidis; and (iii) a method for preventing and for treating an infection with pathogenic Neisseria strains, in particular with Neisseria meningitidis, by administering a therapeutic or prophylactic amount of said polynucleotide to an individual requiring such a treatment.

The polynucleotides of the invention (DNA or RNA) can be administered to a vertebrate as they are. When a DNA molecule of the invention is used, it can be in the form of a plasmid incapable of replicating in a vertebrate cell and incapable of integrating the genome of said vertebrate. Said DNA molecule is, typically, placed under the control of a promoter suitable for expression in a vertebrate cell. Said polynucleotide used as vaccine can be formulated according to various methods known to those skilled in the art. Said polynucleotide can, in particular, be used in a naked form, free of any vehicle which promotes transfer to the target cell, such as anionic liposomes, cationic example gold microparticles, for microparticles, precipitation agents, for example calcium phosphate, or any other agent which facilitates transfection. In this case, the polynucleotide can be physiologically acceptable simply diluted in а solution, such as a sterile solution or a sterile

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buffer solution, in the presence or absence of a vehicle. When it is present, this vehicle can be preferably isotonic, hypotonic or slightly hypertonic, and has a relatively low ionic strength. It can, for example, be a sucrose solution (for example a solution containing 20% of sucrose).

Alternatively, a polynucleotide of the invention can be combined with agents which facilitate transfection. It can be, inter alia, (i) combined with a chemical agent which modifies cell permeability, such as bupivacain (WO 94/16737); (ii) encapsulated in liposomes, optionally in the presence of additional substances which facilitate transfection (WO 93/18759, WO 93/19768, WO 94/25608 and WO 95/2397, WO 93/18759 and WO 93/19768); or (iii) combined with cationic lipids, or silica, gold or tungsten microparticles.

When the polynucleotides of the invention coat microparticles, these particles can be injected via the intradermal or intraepidermal route, using the "gene gun" technique (US 4,945,050, US No. 5,015,580 and WO 94/24263).

The amount of DNA to be used as a vaccine depends, in particular, on the strength of the promoter used in the DNA construct, on the immunogenicity of the product expressed, on the individual to which this DNA is administered, on the method of administration and on the type of formulation. In general, a therapeutically or prophylactically effective amount ranging from approximately 1 µg to approximately 1 mg, preferably from approximately 10 µg to approximately 800 µg, and preferentially from approximately 25 µg to approximately 250 µg, can be administered to human adults.

The polynucleotide of the invention can he conventional route of administered via any 35 in particular the such as via administration, of choice of the route parenteral route. The particular, the depends. in administration formulation chosen. A polynucleotide formulated in

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combination with bupivacain is advantageously administered into muscle. When neutral or anionic liposomes, or a cationic lipid such as DOTMA (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium

chloride) or DC-Chol (3-beta-(N-(N',N'-dimethyl-aminomethane)carbamoyl)cholesterol) are used, the formulation can advantageously be injected via the intravenous, intramuscular, intradermal or subcutaneous route. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal or subcutaneous route.

The nucleotide sequences of the invention allow the construction of specific nucleotide probes and primers which can be used in diagnosis. Said probes or primers are nucleic acids having sequences identical or homologous to portions of the sequences of group I or to the sequences complementary thereto.

probes contain from Preferably, said approximately 5 to approximately 100, preferably from approximately 10 to approximately 80, nucleotides. They can contain modified bases, the sugar and phosphate residues possibly also being modified or substituted. The probes of the invention can be used in diagnostic tests, to capture or detect polynucleotides specific for pathogenic Neisseria strains. Such capture probes can conventionally be immobilized on a solid support directly or indirectly, by covalent bonding or by passive adsorption. A detection probe can be labelled, in particular with a radioactive isotope, an enzyme such as peroxidase or alkaline phosphatase, or enzymes capable of hydrolyzing a chromogenic, fluorogenic or luminescent substrate, or with compounds which are, themselves, chromogenic, fluorogenic or luminescent, nucleotide analogues; or biotin.

A primer generally contains from approximately 10 to approximately 40 nucleotides, and can be used to initiate enzymatic polymerization of the DNA in an amplification process (for example PCR), in an elongation process or in a reverse transcription

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method. A primer of the invention can in particular be a primer as described in Example II.1 hereinafter.

A subject of the present invention is also:

- (i) a reagent containing a probe of the invention for detecting and/or identifying the presence of pathogenic Neisseria strains in a biological sample;
 - (ii) a process for detecting and/or for identifying the presence of pathogenic Neisseria strains in a biological sample, said method comprising the steps consisting in a) extracting the DNA or RNA from a biological sample and denaturing it; b) exposing said DNA or said RNA to a probe of the invention, under stringent hybridization conditions, so as to detect the hybridization; and
- (iii) a method for detecting and/or for identifying pathogenic Neisseria strains in a biological sample, in which the DNA is extracted from a biological sample and mixed together with at least one and preferably with two primers of the invention, and is amplified, for example by PCR.

As mentioned above, the polypeptides produced by the expression of the ORF sequences identified can specific as vaccination agents. The used antigenicity of the polypeptides homologous to the polypeptides having sequences of group II evaluated by assaying the cross-reactivity with an antiserum directed against the polypeptides having sequences of group II. A monospecific hyperimmune against a purified be produced antiserum can polypeptide having a sequence of group II or a fusion polypeptide, for example an expression product of the MBP, GST or His-tag systems.

The specific antigenicity can be determined using various methods known to those skilled in the art, in particular the Western blot, dot blot and ELISA techniques, described below.

In the Western blot technique, the protein preparation to be tested is subjected to SDS-PAGE gel electrophoresis. After transfer onto a nitrocellulose

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membrane, the material is incubated with a monospecific hyperimmune antiserum obtained after having immunized an animal with the referent material; i.e., in the present case, with a polypeptide having an amino acid sequence of group II. This antiserum is diluted beforehand in a dilution range of approximately 1:50 to 1:5000, preferably of approximately 1:100 to 1:500. The specific antigenicity is revealed when a band corresponding to the product shows reactivity with one of the dilutions above.

a purified protein the ELISA assay, Tn preparation is preferably used, although a whole cell extract may also be used. Approximately 100 μl of a preparation at approximately 10 $\mu g/ml$ are distributed into the wells of a plate. The plate is incubated for two hours at 37°C, and then overnight at 4°C. The plate then washed with a phosphate buffered saline solution (PBS) comprising 0.05% of Tween 20. The wells are saturated with 250 µl of PBS containing 1% of bovine serum albumin (BSA) so as to prevent nonspecific antibody binding. After incubation for one hour at 37°C, the plate is washed with the PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100 μl of this dilution are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is carried out for 90 minutes at 37°C and the plate is then washed. The reaction is measured by colorimetry (the reaction is positive when the optical density value is 1, if the dilution is at least 1:50, preferably at least 1:500).

In the dot blot assay, a purified protein is preferably used, it being understood that it is also possible to use a whole cell extract. Two-fold serial dilutions of a protein solution at approximately 100 $\mu g/ml$ are prepared in a 50 mM Tris-HCl buffer,

pH: 7.5. 100 μl of each dilution are applied to a nitrocellulose membrane (BioRad apparatus). The buffer is removed by applying suction to the system. The wells are washed by adding 50 mM of Tris-HCl buffer (pH: 7.5) and the membrane is air-dried. The membrane is then saturated in a blocking buffer (50 mM Tris-HCl (pH: 7.5) 0.15 M NaCl, 10 g/l of skimmed milk) incubated with a dilution of antiserum ranging from 1:5000, preferably 1:50 to approximately approximately 1:500. The reaction is revealed 10 accordance with standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is carried out for 90 minutes at 37°C. The reaction is developed with the suitable substrate 15 and measured, for example by colorimetry, by the appearance of a coloured spot (a reaction is positive when a coloured spot appears in association with a dilution of at least 1:50, preferably of at least 1:500). 20

A subject of the present invention is also (i) composition containing pharmaceutical therapeutically or prophylactically effective amount of a polypeptide of the invention; (ii) a method for pathogenic response against 25 inducing an immune Neisseria strains in a vertebrate, by administering to said vertebrate an immunogenically effective amount of a polypeptide of the invention so as to cause an immune response, in particular a protective immune response against pathogenic Neisseria strains; and 3.0 method for preventing and/or for treating an infection with pathogenic Neisseria strains, by administering a therapeutic or prophylactic amount of a polypeptide of the invention to an individual requiring such a treatment. 35

The immunogenic compositions of the invention can be administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous,

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intradermal, intramuscular, intravenous or intraperitoneal route). The choice of the route of administration depends on a certain number of parameters, such as the adjuvant combined with the polypeptide.

A composition of the invention contains at least one polypeptide as defined above. It can also contain at least one additional antigen of Neisseria meningitidis and/or Neisseria gonorrhoeae.

The polypeptides of the invention can be formulated with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS or "virus-like" particles, in order to facilitate the transfer of the polypeptide and/or to increase the immune response.

The administration can be carried out with a single dose or with doses repeated, if necessary, at intervals which can be determined by those skilled in the art.

For example, an initial dose can be followed by three booster doses at intervals of one or more weeks 20 or of one or more months. The suitable dose depends on many parameters, including the individual treated (adult or child), the specific vaccination antigen, the route of administration and the frequency 25 administration, the presence or absence or the type of desired and the effect (for protection and/or treatment), and can be determined by those skilled -- in the art. Ιf the route of... administration is parenteral, the dose preferentially less than 1 mg, preferably approximately 30 100 µg. The polypeptides and polynucleotides of the invention used as vaccination agents can be used sequentially, in a several-step immunization process. For example, a vertebrate can be initially sensitized 35 with a vaccination vector of the invention, such as a poxvirus, for example via the parenteral route, and can then be stimulated twice with the polypeptide encoded

by the vaccination vector.

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A polypeptide of the invention can also be useful as a diagnostic agent for detecting the presence of anti-Neisseria meningitidis and/or anti-Neisseria gonorrhoeae antibodies in a biological sample such as a blood sample.

A subject of the present invention is also monospecific antibodies directed against the polypeptides of the invention.

The term "monospecific antibodies" is intended to mean an antibody capable of reacting specifically with a Neisseria polypeptide of the invention. Such antibodies can be polyclonal or monoclonal, and can be recombinant antibodies, for example chimeric (for example consisting of a variable region of murine origin associated with a constant region of human origin), humanized and/or single-chain antibodies. Said antibodies can also be in the form of immunoglobulin fragments, for example F(ab)'2 or Fab fragments. The antibodies of the invention can be of any isotype, for example IgA or IgG, the polyclonal antibodies possibly being of a single isotype or possibly containing a mixture of several isotypes.

The antibodies of the invention directed against the polypeptides of the invention can be produced and identified using standard immunological methods, for example Western blot analysis, a dot blot assay, an ELISA assay (Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). Said antibodies can be used in diagnostic processes for detecting the presence of a Neisseria meningitidis antigen in a sample such as, in particular, a biological sample (for example a blood sample).

The antibodies of the invention can also be used in affinity chromatography processes for purifying a polypeptide of the invention. Finally, such antibodies can also be used in prophylactic or therapeutic passive immunization methods.

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A subject of the present invention is also a diagnostic method for detecting the presence of pathogenic Neisseria strains in a biological sample, comprising bringing said biological sample into contact with an antibody or a polypeptide of the invention, such that an immune complex is formed, and detecting said complex which indicates pathogenic Neisseria strains in the organism from which the sample originates. Those skilled in the art understand that the immune complex is formed between a component of the 10 sample and the antibody or the polypeptide of the invention, any substance not bound possibly being eliminated prior to the detection of the complex.

Thus, a reagent of polypeptide type can be used the presence of anti-Neisseria for detecting meningitidis and/or Neisseria gonorrhoeae antibodies in a sample, whereas an antibody of the invention can be used as a reagent for assaying the presence of a Neisseria meningitidis and/or Neisseria gonorrhoeae polypeptide in a sample.

For use in diagnostic applications, the reagent (for example the antibody or the polypeptide of the invention) can be in the free state or immobilized on a solid support, by direct or indirect means.

The direct means include passive adsorption or covalent bonding between the support and the reagent.

The term "indirect means" is intended to mean that a substance which interacts with said reagent is attached to the solid support. For example, if a reagent of polypeptide type is used, an antibody which binds to this polypeptide can be used as an antireagent substance, it being understood that this substance binds to an antibody which is not involved in recognizing the antibodies in the biological samples.

Among the indirect means which can be used, mention may also be made of the ligand receptor system, a molecule such as a vitamin possibly being grafted reagent of polypeptide type, and the corresponding receptor possibly being immobilized on

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the solid phase. This is illustrated by the biotinstreptavidin system. It is also possible to add a peptide tail to the reagent, by chemical engineering or genetic engineering, and to immobilize the grafted or fused product by passive adsorption or covalent bonding with the peptide tail.

A subject of the present invention is also a process for purifying, from a biological sample, a Neisseria polypeptide of the invention, by affinity chromatography with a monospecific antibody of the invention. Said antibody is preferably of isotype IgG.

According to an example of implementation, a biological sample, preferably in a buffer solution, is applied to a chromatographic material, preferably equilibrated with the buffer used to dilute the biological sample, such that the polypeptide of the invention (i.e. the antigen) may adsorb to the material. The unbound components are washed and the antigen is then eluted with a suitable elution buffer, such as a glycine buffer or a buffer containing chaotropic agent, for example guanidine HCl, or a high concentration of salt (for example 3 M MgCl₂). The eluted fractions are recovered and the presence of antigen is detected, for example by measuring the absorbence at 280 nm.

A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a monospecific antibody of the invention; and (ii) a method for preventing and/or for treating an infection with pathogenic Neisseria strains, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an individual requiring such a treatment.

To this end, the monospecific antibody of the invention is preferably of isotope IgG, and preferably fixes the complement. Said monospecific antibody according to the invention can be administered alone or in a mixture with at least one other monospecific

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antibody, specific for a different Neisseria meningitidis and/or Neisseria gonorrhoeae polypeptide, according to the invention. The amount of antibody can be determined easily by those skilled in the art. For example, a daily administration of approximately 100 to 1000 mg of antibodies over a week, or three daily doses of approximately 100 to 1000 mg of antibodies over two or three days, may be an effective dose.

The therapeutic or prophylactic effectiveness may be evaluated using standard methods known to those skilled in the art, for example by measuring the induction of an immune response or the induction of protective and/or therapeutic immunity (in newborn rats or mice), through evaluation of the bacterial load in the cerebrospinal fluid. The protection can determined by comparing the degree of Neisseria control infection to а group. Protection demonstrated when the infection is decreased in comparison with the control group. Such an evaluation can be carried out with the polynucleotides, the vaccination vectors, the polypeptides and also the antibodies according to the invention. The therapeutic or prophylactic effectiveness of a product according to the invention (polynucleotide or polypeptide) can also be evaluated in an assay for bactericidal activity, as described by Danve et al., Vaccine (1993) 11(12):1214 against the meningococcal strain of origin of the polynucleotide or polypeptide used. In the field of meningococcal vaccines, the bactericidal activity assay is, in fact, recognized as being the reference assay based upon which it is possible to make a valid prediction of the vaccination value of a product. Briefly, a product according to the invention is administered to animals such as rabbits in order to produce an antiserum against this product. Then, this antiserum is assayed for its lysis capacity. The bactericidal titre of an antiserum represents the inverse of the dilution of this antiserum for which 50% of the load of meningococci is lysed. The antiserum is

considered to be bactericidal when the titre is higher than 4, with respect to the menigococcal strain of origin of the polynucleotide or polypeptide used. In that case, the product against which the antiserum was generated is demonstrated to be potentially advantageous from a pharmaceutical point of view.

The following examples illustrate the invention without limiting the scope thereof.

Legend of the figure

The attached figure represents the vector pCAMyc-His used as a cloning vector.

Details of the strategy for identifying the

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In order to select the ORF sequences specific for the pathogenic strains of the Neisseria genus, a PCR amplification is carried out on the sequences of the 118 ORFs selected after analysis with the Gene Jockey®, Codon Use®, and homology search programs. Only the sequences for which the amplification in N. lactamica is negative (sequences named "lactamica") are selected. In order to verify that these negative results are not "false negatives", the lactamica sequences selected are subjected to a dot blot.

A - PCR amplification:

A.1. Extraction of genomic DNAs:

The genomic DNAs of all of the Neisseria strains used in this study were prepared according to an identical protocol. The N. meningitidis, N. lactamica, N. flava, N. subflava and N. mucosa strains were cultured on tissues of MHA (Muller Hinton Agar, Difco) medium, and the N. gonorrhoeae were cultured on tissues of MHA medium supplemented with 10% of heat-treated horse blood (Biomérieux) and 1% of Isovitalex (Biomérieux). The culturing is carried out under an atmosphere containing 10%

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CO₂, overnight at 37°C. Then, the cells are harvested, and washed in PBS phosphate buffer (pH 7.2), and the DNA is extracted according to protocol D of the "Rapid Prep genomic DNA isolation kit for cells and tissue" (Pharmacia Biotech).

The genomic DNAs were then controlled on agarose gel for their completeness and by PCR reaction for their purity.

10 A.2. PCR reaction for screening the ORFs absent in N. lactamica 2314:

A PCR amplification was carried out on the genomic DNAs of the N. meningitidis strain ATCC 13090 and N. lactamica strain 2314 (ATCC 23970), according to the following protocol:

The PCR reaction was carried out on a 50 μ l volume with 10 ng of genomic DNA, 250 μ M of each of the dNTPs, 300 nM of each of the primers, 1% Taq DNA polymerase buffer and 2 u of Taq DNA polymerase (Appligène).

The amplification cycles are:

	97°C	45 seconds	25 cycles
25	56°C	1 minute	25 cycles
	72°C	2.30 minutes	25 cycles

For each of the ORFs analysed, positive and negative controls for the PCR reaction were carried out. At this stage, only the N. meningitidis+ and N. lactamica- ORFs are selected.

B - <u>Selection of the N. meningitidis*</u> N. lactamica ORFs by dot blot on genomic DNA:

The absence of a product of PCR amplification of an ORF with genomic DNA of N. lactamica 2314 as the matrix does not guarantee the absence of this ORF in the N. lactamica 2314 genome. Specifically, a certain variability in the region to which the oligonucleotides

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should hybridize may be responsible for the absence of amplified product for a given ORF.

this context, further verification carried out by dot blot on genomic DNA, using, as probe, the products of genomic amplification on the N. meningitidis strain corresponding to each of the reading frames identified. The dot blot filters contain genomic DNA of the following strains: 2 N. lactamica strains 8064 and 2314, one N. flava strain ATCC 30008, one N. mucosa strain ATCC 9297, 3 N. meningitidis 10 serogroup B strains ATCC13090, M982 and B16B6, N. meningitidis serogroup Α strain 72491. one N. meningitidis serogroup C strain (strain Z4182) and 2 N. gonorrhoeae strains MS11 and FA1090. This dot blot analysis makes it possible to validate the absence of the ORF in N. lactamica 2314 and 8064, and it is also an indication of the degree of variability of an ORF within the Neisseria strains.

The dot blot technique used is as follows. Approximately 50 ng of genomic DNA, denatured for 5 min at 100°C, of the various Neisseria strains are loaded, with suction, onto a Hybond N+ nitrocellulose membrane (Amersham) placed between the jaws of a dot blot apparatus (BioRad). Then, the DNA is fixed on the membranes for 5 min with UV radiation at 315 nm.

The membranes are incubated in a prehybridization buffer (containing denatured salmon sperm DNA). They are then hybridized with a probe corresponding to the product of amplification of the ORF of interest, labelled according to a cold labelling protocol, such as the "DIG DNA labelling and detection kit" system (Boehringer Mannheim).

The ORF which does not hybridize to the genomic DNA of N. lactamica 2314 and 8064 is definitively selected as a potential vaccination candidate.

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Example I: Cloning

1. PCR amplification

Each of the ORFs was amplified by PCR using the genomic DNA of N. meningitidis serogroup B (strain ATCC 13090), according to standard protocol.

Two oligonucleotides, primers on the N-terminal side and on the C-terminal side were defined for each of the ORF sequences of the invention.

The primer on the N-terminal side comprises an enzyme restriction site for cloning, a CCACC Kozak sequence for translation initiation (M. Kozak, J. Mol. Biol. 196: 947-950), the ATG of the potential ORF and approximately 17 bases specific for the 5' portion of the ORF.

The primer on the C-terminal side was defined such that the ORF cloned is in fusion, in its 3' portion, with a repeat of 8 histidines and a stop codon which are present in the vector behind the multiple cloning site, hence the insertion of an "A" base in order to keep the correct reading frame after cloning and the disappearance of the stop codon of the ORF. The primer on the C-terminal side thus comprises an enzyme restriction site for cloning, an "A" base, and then approximately 20 bases specific for the 3' portion of the gene starting from the codon preceding the stop codon.

After searching for restriction sites which are absent in each of the ORFs, with the aid of the DNASTAR 30 MapDraw subprogram (Lasergene Software), the XbaI restriction site in 5' and BglII restriction site in 3' are used for the ORF SEQ ID No. 19. For the ORF SEQ ID No. 41, the SpeI site in 5' and the BglII site in 3' are used. The XbaI restriction site in 5' and BamHI restriction site in 3' are used to clone the remaining ORFs.

The PCR mixture comprises, for a final volume of 100 $\mu\text{l}\,,$ 10-50 ng of genomic DNA, the N-terminal and C-terminal primers each at 200 nM, the dNTPs each at 250 μ M, the 1X PCR buffer (composition of the 10X PCR buffer: 200 mM Tris-HCl (pH 8.8), 20 mM MgSO₄, 100 mM KCl, 100 mM (NH₄)₂SO₄, 1% TritonX-100 and 1 mg/ml of nuclease-free bovine serum albumin) and 2.5 U of polymerase.

The amplification is carried out as follows:

Step	Temperature	(°C)	Time	(min.)	Number	of
					cycles	
Denaturation	97		0.45		25	
Hybridization	cf. table		1		25	
Elongation	72		1/kb	DNA	25	

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The primers used and the PCR conditions given in the table below, in which "N. g allelic variant" means that an allelic variant is present in Neisseria gonorrhoeae and "N. m A allelic variant" means that an allelic variant is present in Neisseria meningitidis serogroup A.

ORF No.	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization
(internal					٦.
ref.)			CILL I DO INCO COM		
22	1-2	GCT CTA GAC CAC CAT GIC TGA AUA	CGG GAT CCA GAA ATG GCT GGA TTC GCT ATC AG (SEOID nº 79)	Tfu	ວ.95
	N.g allelic variant:	Non Maria Caracteria C		(Appligene)	
	54, 55				
11	3-4	OCT CTA GAC CAC CAT GAA ACA CTT COG GAT CCA ATA CGT AGG ACT TGG	CGG GAT CCA ATA CGT AGG ACT TGG	Tfu	43°C
ř	1	ACT CAT CG (SEQ ID nº 80)	GTC (SEQ ID n° 81)	(Appligene)	
4.0	2-3	GCT CTA GAC CAC CAT GAA AAA ATC	CGG GAT CCA TTG CGG ATA AAC ATA	Tfu	2,95
47-43	ח	CCT TTT CGT TC (SEQ ID nº 82)	TTC CGC C (SEQ ID n° 83)	(Anny i Cane)	
	N.g allelic variant:			(anaStrdde)	
	56, 57				
47	7-8	'AC GAC	CGG GAT CCA GAA CCG GTA GCC TAC	Lfu	26°C
	N.g allelic variant:	ככב עער כדון כי (פעל וויי וו פען		(Appligene)	
	58, 59		Co. Com co.		
55	9-10	GCT CTA GAC CAC CAT GAA CAC ACG	CGG GAT CCA GCA ACG GCC INC CGC TIT AAG (SEO ID nº 87)	Pfu Turbo	26°C
	N.g allelic variant:	CALCATOR TO THE TARK THE		(Stratagene)	
	60, 61		CO		
89	11-12	AC GIT	CGG GAT CCA CGG CAG AGG CAC GAT	rfu	2,95
)		TATCGG ACT G (SEQ ID n° 88)	ICC (Such ion see	(Appligene)	

CYCSCASS COASSA

ORF No.	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization
(internal			.,1-		+
161.)	2. 6.	GCT CTA GAC CAC CAT GGG CAT CCA	CGG GAT CCA CAA AAG TTC CAG AAA	Tfu	2,95
1/	#T - CT	TCF CGA CTF C (SEQ ID In 90)	ATC TAA CTC (SEQID n° 91)	(Appligene)	
12	15-16	GCT CTA GAC CAC CAT GAA TAG ACC	CHO GAT CCA TGC CGC TTG GGG GAG GC	Pfu Turbo	2e9G
7	N.mA, allelic	CAA GCA ACC (SEQ ID n° 92)	(SEQ II) n° 93)	(Stratagene)	
	variant: 62, 63		The state of the s		
73	17-18	GCT CTA GAC CAC CAT GAT GAA TGT CGA GGC AGA G (SEO ID nº 94)	CGG GAT CCA CAG TTT GCC CGA CAT AC (SEO ID nº 95)	Pfu Turbo	26,00
	N.g allelic			(Stratagene)	
	variant:				
	64, 65				
74	19-20	GCT CTA GAC CAC CAT GAA ATT TIT	GAA GAT CTA GAA ACT GTA ATT CAA	Pfu Turbo	2,95
		(a) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c		(Stratagene)	
o	21-22	GCT CTA GACCACCAT GAT TGA ATT	CGG GAT CCA ACC CIG CGA CGA GIT	Pfu Turbo	2e9G
000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	rg r ccg agc (SEQ ID n° 98)	GCG (SEQ ID n° 99)	(Stratagene)	
116	23-24	GCT CTA GAC CAC CAT GCA ATA CAG	CGG GAT CCA GTC CFF TITT CGC ACC TTG	Pfu Turbo	26°C
) 	N.g.allelic	CAC ACI CINC (SEQ II) II 1993	VVG (305 (10.11) 10.1)	(Stratagene)	
	variant:				
	66, 67				
122	25-26	GCC CTA GAC CAC CAT GGA GCA GTC	CGG GAT CCA AGC TGT THG GCG ATT	Pfu Turbo	26°C
		(and and bould a life wood poor		(Stratagene)	
	With the Party of				

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				operom.log	Hybridization
ORF No.	SEQ ID No.	5' Primer	3' Primer	FOTYMETERS	°L
(internal					
ref.)		900 *** 1,000	COS CAT OCA CTG OCT GOG CAG CIT	Dfr Turbo	2,9€
125	27-28	CCC CCC AAA GC (SEQ ID n° 104)	GGA ATC (SEQ ID nº 105)	(Stratagene)	
		100 tar oromoo o o o	CCG GAT OCA TIC CGC AAA TAC CTG	TF11	2,95
128	29-30	CAA TCT AAT CAT AAT G (SFQ ID #* 106)	TITI CCA ACC (SEQ ID nº 107)	(anepilana)	
	N.mA. allelic			(arragarday)	
	variant: 68, 69		*34 *30 333 OHL O'H - 35		0070
031	31-32	GCT CTA GAC CAC CAT GAA ACA ATC	CGG GAT CCA TAC 110 GGC GCA ACA	ogini nid	200
777	w ~ 11elic wariant.	Contractor and Contractor		(Stratagene)	
	N.9 attette tarrain				
	70, 71	ATT TOT AND TAX OLD CASE OF THE PROPERTY OF TH	COG GAT CCA TIT TITI AGA CGT ATT TIT	TF11	2,9€
153	33-34	CGC T11 CCC (SFQ II) n° 110)	AGT CG (SEQ ID nº 111)	(Appligene)	
		CCT CTA CAC CAC CA F GAT GAG TCA	CGG GAT CCA TOC AGT 11T TGC TCG	Tfu	2,95
155	35-36	ACA CTC FGC C (SEQ ID nº 112)	AAG GC (SEQ 1D n° 113)	(Appligene)	
		GCT CTA GAC CAC CAT GCC TTC GAG	CGG GAT CCA TCG TTC TTC AAT CTC CAC	nji	26°C
156	37-38	CAA AAA CTG G (SEQ ID nº 114)	AAA CG (SEQ 1D nº 115)	(Appligene)	
		DJ VJ9 J.V.J JVJ JVI VIII IDO	COMPANY CAS CAST GCA CCT CGG GAT CCA THE AAT TEG CIT CAA	Tfu	20,9€
157	39-40	TGG AAA G (SEQ ID nº 116)	CAA TG (SEQ ID n" 117)	(Appligene)	

					was the state of the state of
ORF No.	SEQ ID No.	5' Primer	3' Primer	Ролумегаве	mybridización
(internal					-
ref.)			CEE		
158	41-42	GGA CTA GTC CAC CAT GGC TGC CAA	GAA GAT CIA AGC CGC GIT CCC LIC	Tfu	26°C
9	N.mA. allelic	כרא עכם ווע נכם (מכלוות ויים)	CAA AAA ATC (SISCID II 112)	(Appligene)	
	variant: 72. 73				
0	43-44	GCL CTA GAC CAC CAT GCC GCA AAT	CGG GAT CCA AAA ACA AIC ITC CGG	Tfu	2,9€
T C		TAA AAT TCC (SEQ ID nº 120)	CACCC (SEQ ID nº 121)	(Annigone)	
	N.mA. allelic			(Appridate)	
	variant: 74, 75				
171	76-76	GCF CTA GAC CAC CAT GCG CAC GCC	_	Ifn	26°C
тот	0.5	GTT TTG TTG (SEQ 10 nº 122)	GGC AC (SEQ ID n° 123)	(Appligene)	
		6.0	222 21 TTC TCC 4 AT CCT TTC TCC	- F	7000
163-1	47-48	_	CGG GAT CCA TOUCHC AND CCT TTC TOC	ogani nid)_9c
		AGA GAT CAC ACC (SEQ ID II- 124)	(221 11 711)(26)	(Stratagene)	
0	C L	GCT CTA GAC CAC CAT GAT TCA CGT	CGG GAT CCA ACC TGC TTC ATG GGT	Tfu	26°C
163-2	4 2 - 50	TTC GGC AGT G (SEQ ID n° 126)	(ATTC (SEQ ID n° 127)	(Appligene)	
		GCT CTA GACCACCAT GAA TIC GAC	CGG GAT CCA AAT CCC TCT GCC GTA	Tfu	2,95
Te7-168	25-TC	CGC AAG TAA AAC (SEQ ID nº 128)	111f G (SEQ II) nº 129)	(Output Frank)	
	N.gallelic variant:			(апабттдач)	
	76, 77				
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2- Cloning, transformation and selection of recombinants

The cloning vector used is the 6.357 kb vector. pCA/Myc-His or pM1070 (cf. figure), derived from the plasmid pCDNA 3.1 (Invitrogen). pCA/Myc-His comprises, in particular, the CMV iel promoter (bases 249-902), intron A of the CMV iel gene (Chapman et al., 1991 Nucleic Acids Research, 19, 3979-3986), a multiple cloning site (bases 1792-1852) with the PmlI, EcoRV, NotI, XbaI, BamHI, KpnI and HindIII sites, a sequence encoding a polyhistidine and a stop codon (bases 1908-1928), a bgh 3' termination sequence (bases 1853-2197) and the ampicillin resistance gene for selecting the recombinant clones in E. Coli

selecting the recombinant clones in E. coli.

After purification (GeneClean Biol01 kit), the PCR amplification products are digested for 2 hours at 37°C with the appropriate enzymes (XbaI-BamHI, XbaI-BglII or SpeI-BglII), in a final reaction volume of 20 µl. The digestion products are then ligated with the vector pCA/Myc-His, digested beforehand with XbaI and BamHI, according to the "Rapid DNA Ligation Kit" protocol (Boehringer Mannheim). 15 µl of the ligation is used to transform 100 µl of competent E. coli XLI-blue cells (Novagen). The cells are incubated for 30 minutes in ice, 30 seconds at 42°C and 2 minutes in ice. Then, 500 µl of LB medium without antibiotics are added, and the mixture is incubated for 1 hour at 37°C. Next, 50 and 550 µl of the culture are plated out on

final concentration), and incubated overnight at 37°C. The following day, 36 colonies are placed in culture in 2 ml of LB plus ampicillin (50 μ g/ml) and incubated overnight at 37°C.

plates containing LB medium plus ampicillin (50 µg/ml

The following day, the plasmid DNA is extracted
according to the Qiagen mini-prep protocol (Qiagen) and
the recombinants are identified by enzymatic
restriction followed by agarose gel electrophoresis.
The cloning junctions are then verified by sequencing.

Example II: Evaluation of the protective activity of the ORFs of the invention

Preparation of the DNA intended for the immunization experiments:

An isolated colony of a recombinant clone is to inoculate a preculture in LB medium + ampicillin, and 5 ml of this preculture represents the inoculum of a 2.5 litre culture in LB medium + 10 ampicillin. The purification protocol for preparing the plasmid DNA is that described in the EndoFree Giga Kit (Oiagen). The purified DNA is eluted from purification column with a 10 mM Tris-HCl, 1 mM EDTA buffer, pH 8, and stored at -20°C. Before injection, the purified recombinant plasmid is diluted injectable preparation (of 100 μg/ml with water quality) and the NaCl concentration is brought to 150 mM.

Production of a specific polyclonal serum:

Hyperimmunization in an animal model: The animal model used is the mouse or the 25 rabbit. The route of administration of the injected DNA the intramuscular or intradermal route. recombinant plasmids to be injected are optionally applied to beads if they are injected into animals using a gene gun apparatus (BioRad). The immunization 30 protocol follows a scheme comprising two injections, 3

Analysis of the bactericidal activity of the antibodies induced:

Ten days after the final injection, the animals and the sera are analysed using the bactericidal activity assay according to the protocol of Danve et al., Vaccine (1993) 11 (12):1214. Briefly,

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weeks apart.

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the sera are incubated at various dilutions (2-fold) in the presence of rabbit complement and of meningococci cultured in the presence or absence of an iron-chelating agent. The bactericidal titre of a serum represents the inverse of the dilution of this antiserum for which 50% of the bacteria are lysed.

It is considered that the antiserum is not bactericidal when its titre is lower than 4 against the homologous strain.

When the bactericidal titre corresponds to a 4-fold seroconversion against the homologous strain, the bactericidal activity of the antiserum is analysed against other Neisseria strains in order to measure the extent of the cross-reactivity of the antiserum of interest.

Example III: Production of purified recombinant proteins

Recombinant production of proteins

a. Preparation of transformants:

The PCR product obtained is then digested at 37°C for two hours with restriction enzymes, in 20 μl of reaction volume. The digestion product is ligated into a plasmid pET28a (Novagen) which is cleaved in a similar way and which is dephosphorylated, before ligation, by treating with calf intestine alkaline phosphatase. The fusion gene constructed in this way allows the one-step affinity purification of the resulting fusion protein, due to the presence of histidine residues at the N-terminal end of the fusion protein, which are encoded by this vector.

The ligation reaction (20 µl) is carried out at 14°C overnight, before transforming 100 µl of fresh competent *E. coli* XL1-blue cells (Novagen). The cells are incubated on ice for two hours, and then subjected to a heat shock at 42°C for 30 seconds, before being returned to the ice for 90 seconds. The samples are

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then added to 1 ml of LB broth without selection, and cultured at 37°C for two hours. The cells are then plated out on LB agar medium supplemented with kanamycin (50 $\mu g/ml$ final concentration) at a 10x dilution, and are incubated overnight at 37°C. The following day, 50 colonies are subcultured on secondary plates and are incubated at 37°C overnight.

b. Production of the protein:

The stored transformants (10 μ l) are plated out onto selection plates and cultured overnight at 37°C. A few cells are harvested from the plate and used as an inoculum for an overnight starter culture (3 ml) at 37°C. The following day, a sample (time T=0) is taken and centrifuged at 14 000 rpm for 3 minutes. starter culture is then used to inoculate an LB medium containing kanamycin (100 $\mu g/ml$) at a dilution of 1:50 (starting optical density $OD_{600} = 0.05-0.1$). The cells are cultured to an OD_{600} of 1.0, a sample is taken for SDS-PAGE (pre-induction sample) and the remaining culture is induced with 1 mM of IPTG. The cultures are cultured for four hours and samples are taken every hour. The culture is centrifuged at 600 q for 20 minutes at 4°C. The supernatant is discarded and the pellets are resuspended in 50 mM of Tris-HCl (pH: 8.0), 2 mM EDTA, and recentrifuged. The supernatant is discarded and the cells are stored at -70°C.

Protein purification

The pellets obtained from one litre of culture prepared according to Example I.4 above are dried and resuspended in 20 ml of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 5 mM imidazole, cooled in ice. Lysozyme is added at a concentration of 0.1 mg/ml, and the suspension is homogenized using a high-speed homogenizer (Turrax), then treated with a sonicator (Sonifier 450, Branson). Benzonase (Merck) is used at a final concentration of 1 U/ml in order to eliminate the DNA. The suspension is centrifuged at 40 000 g for 20 minutes and the

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supernatant is filtered through a 0.45 μm membrane. The supernatant is loaded onto an IMAC column (12 ml of resin) which has been prepared by immobilizing Ni^{††} cations according to the manufacturer's recommendations (Pharmacia). The column is washed with 10 column volumes of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 60 mM imidazole. The recombinant protein is eluted with six volumes of 20 mM Tris-HCl (pH: 7.9), 0.5 M NaCl, 500 mM imidazole, 0.1% Zwittergent 3-14.

The elution profile is controlled by measuring the absorbence of the fractions at an optical density of 280 nm. An aliquot fraction is analysed on an SDS-PAGE gel and stained with Coomassie blue (Phast System - Pharmacia), and the fractions corresponding to the protein peak are then pooled and concentrated. In order to eliminate the elution buffer, the fraction is passed over a G24 Sephadex column (Pharmacia) and equilibrated in PBS buffer (pH: 7.4). The protein solution is sterilized by filtration through a 0.45 μm membrane, and the protein concentration is determined using the BCA micromethod (Pierce). The protein solution is stored at $-70\,^{\circ}\mathrm{C}$.

Example IV: Production of monospecific

25 polyclonal antibodies

Rabbit hyperimmune antiserum

100 µg (in total) of the polypeptide purified in Example III, in the presence of complete Freund's adjuvant in a total volume of approximately 2 ml, are injected into New Zealand rabbits, both subcutaneously and intravenously. 21 and 42 days after the initial injection, the booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 15 days after the final injection, the animal's serum is recovered, decomplemented and filtered through a 0.45 µm membrane.

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Mouse hyperimmune ascites fluid

10-50 µg of the purified fusion polypeptide obtained in Example II, in the presence of complete Freund's adjuvant, in a volume of approximately 200 μ l, are injected subcutaneously into 10 mice. 7 and 14 days after the initial injection, booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 21 and 28 days after the initial injection, the mice receive 50 μg of the antigen alone, 10 intraperitoneally. On the 21st day, the mice are also injected intraperitoneally with 180/TG CM26684 sarcoma cells (Lennette & Schmidt, Diagnostic procedures for viral, rickettsial, and chlamydial infections, (1979) American Public Washington DC, 5th Ed. 15 Association). The ascites fluids are harvested 10 to 13 days after the first injection.

Example V: Purification of the polypeptides of the invention by immmunoaffinity

Purification of specific IgG

An immune serum as prepared in Example IV is applied to a Fast Flow Sepharose 4 protein A column equilibrated with 100 mM Tris-HCl (Pharmacia) 25 (pH: 8.0). The resin is washed by applying 10 column volumes of 100 mM Tris-HCl and 10 volumes of 10 mM Tris-HCl (pH: 8.0) to the column. The IgGs are eluted with a 0.1 M glycine buffer (pH: 3.0) and are collected by 5 ml fraction, to which 0.25 ml of 1 M Tris-HCl 30 (pH: 8.0) are added. The optical density of the eluate is measured at 280 nm and the fractions containing the IgGs are pooled and, if necessary, stored at -70°C.

Column preparation

A suitable amount of CNBr-activated Sepharose 4B gel (1 g of dried gel providing approximately $3.5~\mathrm{ml}$ of hydrated gel, and the capacity of the gel ranging from 5 to 10 mg of coupled IgG per ml of gel)

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manufactured by Pharmacia (17-0430-01) is suspended in 1 mM HCl buffer and washed, using a Buchner funnel, by adding small amounts of 1 mM HCl buffer. The total volume of the buffer is 200 ml per gram of gel.

The purified IgGs are dialysed for four hours at 20 \pm 5°C against 5 volumes of 500 mM PBS buffer (pH: 7.5). Then, they are diluted in 500 mM of PBS (pH: 7.5) for a final concentration of 3 mg/ml.

The IgGs are incubated with the gel overnight at $5\pm3\,^{\circ}\text{C}$, with stirring. The gel is packed into a chromatography column and washed with 2 column volumes of 500 mM phosphate buffer (pH: 7.5) and then one volume of 50 mM NaCl sodium buffer (pH: 7.5). The gel is then transferred to a tube, then incubated with 100 mM of ethanolamine (pH: 7.5) for 4 hours at room temperature with stirring, and then washed twice with two column volumes of PBS. The gel is then stored in PBS merthiolate at 1/10 000. The amount of IgG coupled to the gel is determined by measuring the optical density at 280 nm of the IgG solution and of the direct eluate.

Adsorption and elution of the antigen

A solution of antigen in 50 mM Tris-HCl 25 (pH: 8.0), 2 mM EDTA, for example the supernatant obtained in Example III.2 after treatment with Benzonase, centrifugation and filtration through a 0.45 µm membrane, is applied to a column equilibrated with 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA, at a flow rate of approximately 10 ml/hour. Then, the column is washed with 20 volumes of 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA. Alternatively, batch adsorption can be carried out, in which the mixture is left overnight at 5 ± 3°C, with stirring.

The gel is washed with 2 to 6 volumes of 10 mM PBS buffer (pH: 6.8). The antigen is eluted with a 100 mM glycine buffer (pH: 2.5). The eluate is collected in 3 ml fractions, to which 150 μ l of 1 mM PBS buffer (pH: 8.0) are added. The optical density is

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measured at 280 nm for each fraction; those containing the antigen are recovered and stored at $-20\,^{\circ}\text{C}$.

(i)

Fragments of the genome of *N. meningitidis* Z2491 described in patent application WO 98/02547

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(2) INFORMATION FOR SEQ ID NO: 70A:

	(B) TYPE: nucleotide	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	•	
	(iii) HYPOTHETICAL: NO	
15		
	(iv) ANTISENS: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70A:	
	GATCAGACCC ATTITCAGCG CACCGIAAGC GCGGATTITC TCGAATTITT CCAAAGCIGC	60
	GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT	120
	CAGGAAAACG GTCGGAATG: CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG	180
	CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG	240
	ATC	243
20		243
	(2) INFORMATION FOR SEQ ID NO: 73A:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 120 base pairs	
	(B) TYPE: nucleotide	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	<pre>(ii) MOLECULE TYPE: DNA (genomic)</pre>	
	(iii) HYPOTHETICAL: NO	

	(iv)	ANTISENS: NO	
_	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 73A:	
5	CGGTCAGAAA CA	GCCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA	60
	ACTCCTTACC GA	AGTOTTOT ATACCOAGGO TOAATAGOOG CTCAAGGAGA GAGOTATOAT	120
	(2) INFORM	ATION FOR SEQ ID NO: 74A:	
10	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
20	(iv)	ANTISENS: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 74A:	
	CGGTCAGAAA CA	GGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA	60
	ACTCCTTACS GA	AGTOTICT ATACCOAGGC TOAATAGCCG CTCAAGGAGA GAGCTATCAT	120
25	(2) INFORM	ATION FOR SEQ ID NO: 77A	
30	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
35	(11)	MOLECULE TYPE: DNA (genomic)	

	(iii) HYPOTHETICAL: NO	
	(iv) ANTISENS: NO	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77A:	
	CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG	6
	ATTTTTATTT CAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA	12
	GAATTCCARC GGGTARAARA GGCCTTGGTR RATTGGCATT ATTCGGGCTT GGCRACARAR	18
	TTGAAATTTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA	24
	TTCGAAGAAG CAAGGGTATT TATCAACCG	26
10	(2) INFORMATION FOR SEQ ID NO: 80A:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(iii) HYPOTHETICAL: NO	
2.0	(iv) ANTISENS: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80A:	
	CGGGTCGCTT TATTITGTGC AGGCATTATT TTTCATTITT GGC7TGACAG TTTGGAAATA	60
	TTGTGTATCG GGGGGGGTA TTTGCTGACG TAAAAAACTA TAAACGCCGC GCAAAATATG	120
	GCTGACTATA TTATTGACTT TGATTTTGTC CTGCGCGGTG ATGGATAAAA TCGCCAGCGA	180
25	TARAGARTT GCGAGARCCT GATGCCG	207

(2) INFORMATION FOR SEQ ID NO: 81A:

(iv) ANTISENS: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81A: 5 CGGCAACGAT TIGAGCTATC GCGGITACGA CATTCTGGAT TIGGCACAAA AATGCGACTT 60 TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120 TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA 18C AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG 224 (2) INFORMATION FOR SEQ ID NO: 87A: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO	5	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 224 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(iv) ANTISENS: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81A: CGGCAACGAT TIGAGCTATC GCGGITACGA CATTCTGGAT TIGGCACAAA AATGCGACTT 60 TGAAGAAGIC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120 TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA 18C AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG 224 (2) INFORMATION FOR SEQ ID NO: 87A: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nuclectide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		(ii)	MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81A: CGGCAACGAT TIGAGCTATC GCGGTTACGA CATTCTGGAT TIGGCACAAA AATGCGAGTT 60 TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120 TTATAAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA 180 AAGCCTGCCT GCACATACCC ATCCGATGGA CGDAATGCGT ACCG 224 (2) INFORMATION FOR SEQ ID NO: 87A: (a) LENGTH: 273 base pairs (b) Type: nucleotide (c) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO	10	(iii)	HYPOTHETICAL: NO	
CGGCAACGAT TIGAGCTATC GCCGTTACGA CATTCTGGAT TIGGCACAAA AATGCGAGTT 60 TGAAGAAGTC 3CCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120 TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA 180 AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG 224 (2) INFORMATION FOR SEQ ID NO: 87A: (a) LENGTH: 273 base pairs (b) TYPE: nucleotide (c) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		(iv)	ANTISENS: NO	
COGGAAGGAT TIGAGCTATC GCCGTTACGA CATTCTGGAT TIGGCACAAA AATGGGACTT TGAAGAAGTC SCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC TTATAAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC COTCTGATTA AAGTTTTGGA AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG (2) INFORMATION FOR SEQ ID NO: 87A: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO	15	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 81A:	
TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG (2) INFORMATION FOR SEQ ID NO: 87A: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		CGGCAACGAT TTG	AGCTATC GOGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT	60
(2) INFORMATION FOR SEQ ID NO: 87A: (3) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		TGAAGAAGTC GCC	CACCTSC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC	120
(2) INFORMATION FOR SEQ ID NO: 87A: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		TTATAAAACC AAG	ECTCANAT CONTGCGCG CCTGCCTNTC CGTGTGNTTN AAGTTTTGGA	180
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		AAGCCTGCCT GCA	ACATACCC ATCCGATGGA CGTAATGCGT ACCG	224
(A) LENGTH: 273 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO		(2) INFORMA	TION FOR SEQ ID NO: 87A:	
(B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO	20	(i)	SEQUENCE CHARACTERISTICS:	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO			(A) LENGTH: 273 base pairs	
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO				
(ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO			-	
(ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO			(D) TOPOLOGY: linear	
	25	(ii)	MOLECULE TYPE: DNA (genomic)	
0 (iv) ANTISENS: NO		(iii)	HYPOTHETICAL: NO	
	30	(iv)	ANTISENS: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87A:		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 87A:	

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC	60
AAAAGCGCGG GGTTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA	120
AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT	180
TGCACACGTT TGGATAAGGA TGCGCGGCGG TTTCAGTATC AAACTGAAAA AATATCCTGC	240
TATGTTTCCA TCAATCGCGC AAACCGATAA ATT	273
(2) INFORMATION FOR SEQ ID NO: 88A:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleotide (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENS: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88A:	
AATTOTTOOG CACGGGGAGG CITGTTTTIC TTCCCTTCTG TTCCGACCGA TTCTCAAATA	60
AAAATCATTG ATTTCATCGA AGTTCATTCC TATACCATTA TCTTTAATAA CGATTTTATG	120
CTCCGGTTTA TCGAATAACC TAACTTCGAC TTCCGTAGCA CATGCATCGT AGGCATTCGC	180
TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTCGA	240
TTACGGTTGG CTCGAAACTC AATTTCAATT	270
(2) INFORMATION FOR SEQ ID NO: 89A:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleotide	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENS: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89A:	
AATTATGAAC ACACGCATCA TCGTTTCGGC TGCGTTCGTT GCGTTGGCAT TAGCAGGTTG	50
CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAAACTT CAGGAACGTG CCGCGTTTGC	120
CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA	180
CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG ITACCAGTGT AATCAGCACA	240
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(A) LENGTH: 308 base pairs	
(B) TYPE: nucleotide	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	

SEQUENCE DESCRIPTION: SEQ ID NO: 94A:

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

ANTISENS: NO

(iv)

(xi)

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(2)

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(A) LENGTH: 286 base pairs	
(B) TYPE: nucleotide	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENS: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95A:	
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AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAACT	180
GACCCTATTG CCATTITATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT	240
AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTGC GGAATT	286

5

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(2) INFORMATION FOR SEQ ID NO: 98A:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs

MOLECULE TYPE: DNA (genomic)

(B) TYPE: nucleotide(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ii)

(iv)	ANTIS	ENS: NO				
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ATGGATAAAA	TOGCCAGOGA	TAAAGATTTG	CGAGAACCTG	ATGCCGGCCT	GTTGTTGAAT	240
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CCCACATTTT	GGAAGC					316

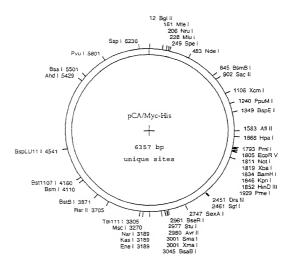
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CLAIMS

- Nucleic acid in isolated form, encoding a polypeptide specific for the pathogenic strains of the
 Neisseria genus, or antigenic fragment thereof, excluding the sequences SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A, the amino acid sequence of said specific polypeptide being identical or homologous to a sequence selected from the
 sequences of group II, group II consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.
 - 2. Nucleic acid according to Claim 1, the nucleotide sequence of which is identical or homologous to a sequence selected from the sequences of group I, group I consisting of the sequences SEQ ID No. 1 to SEQ ID No. 51 (odd numbers).
- Nucleic acid according to Claim 1, encoding a
 polypeptide specific for the pathogenic strains of the
 Neisseria genus, or antigenic fragment thereof, the
 amino acid sequence of said specific polypeptide being
 selected from the sequences SEQ ID Nos 55 to 77 (odd
 numbers).
- Nucleic acid according to Claim 3, having a nucleotide sequence selected from the sequences SEQ ID Nos 54 to 76 (even numbers).
- 5. Polypeptide specific for the pathogenic strains of the Neisseria genus, and antigenic fragments thereof, the amino acid sequence of said specific 30 polypeptide being identical or homologous to a sequence selected from the sequences of group II, consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.

- 6. Polypeptide according to Claim 5, specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (even numbers).
- 7. Expression vector comprising an expression cassette in which a nucleotide sequence as defined in one of Claims 1 to 4 is placed under conditions allowing its expression in a host cell.
- 10 8. Host cell transformed with the expression vector according to Claim 7.
 - Pharmaceutical composition comprising:
- a) a nucleic acid according to one of Claims 1 to 4, in naked form or in combination with at least one
 agent facilitating transfection;
 - b) or a vaccination vector comprising a nucleotide sequence as defined in one of Claims 1 to 4, such as in particular a virus or a bacterium;
- c) or a polypeptide according to either of 20 Claims 5 and 6;
 - optionally in combination with a pharmaceutically acceptable vehicle.
 - 10. Monospecific antibody directed against a polypeptide according to either of Claims 5 and 6.
- 25 11. Use of a nucleic acid according to one of Claims 1 to 4, or of a polypeptide specific for pathogenic Neisseria strains or of antigenic fragments thereof, according to either of Claims 5 and 6, for manufacturing a pharmaceutical composition intended for

1/1



	DECLARATION FOR USA PATENT . (including Design and National Stage PG	
	As a below named inventor, I hereby declare that: My residence, mailing address and citizenship are as stated below adjacent to my name. I believe I a below) or an original, first and joint inventor (if plural names are listed below) of the subject matter win	um the original, first and sole inventor (if only one name is listed ich is claimed and for which a patent is sought
	on the invention entitled: Nucleic acids and polypeptides specific	
	the specification of which: * pathogenic strains	
	is attached hereto.	
	x was filed on 26.04.2001 as U.S. Application No. or PCT I	International Application No. 09/830433
	and (if applicable) was amended on	
	I hereby state that I have reviewed and understand the contents of the above-identified specification, i referred to above. I acknowledge the duty to disclose information which is material to patentability as	
į	I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 355(b) of any foreign application which designated at least one country other than the United States of Americ not claimed, any foreign application for patent or inventor's certificate, or any PCT International application for patent or inventor's certificate, or any PCT International application for patent or inventor's certificate, or any PCT International application for patent or inventor's certificate, or any PCT International Application for patent or inventor's certificate, or any PCT International Application for patent or inventor in the patent of the patent o	tion(s) for patent or inventor's certificate, or 365(a) of any PCT ca, listed below and have also identified below, where priority is ation, having a filing date before that of the application on which
	Prior Foreign Application No. Country	Day/Month/Year Filed Priority Not Claimed
	FR 98 13693 FRANCE	30.10.98
		A CONTRACTOR OF THE PROPERTY O
C	Thereby claim the benefit under 35 U.S.C. 120 of any U.S. application(s), or 365(c) of any PCT application matter of each claims of this application is not disclosed in the prior U.S. or PCT application in the acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR application and the national or PCT filing date of this application ADDITIONAL APPLICATION	ation designating the U.S., listed below; and insofar as the subject he manner provided by the first paragraph of 35 U.S.C. 112, 1 1.56 which became available between the filing date of the prior NS IDENTIFIED ON ATTACHED SHEET.)
iĈ.	U.S. or PCT Parent Application No. Parent Filing Date (Day/Month/Year) Par	rent Patent No. (if applicable)
12	PCTFR99/02643 28.10.1999	
100	As a named inventor, I hereby appoint the registered practitioners of LARSON & TANLOR associated with Customer Number 000881 to prosecute this application and to transact all business Patent and Trademark Office connected therewith. Direct all correspondence to that Customer Number 1	R PLC sin the Customer NS 60881
, LJ	Direct all telephone calls to	
9	I hereby declare that all statements made herein of my own knowledge are true and that all statement further that these statements were made with the knowledge that willful false statements and the like se U.S.C. 1000 and that such willful false statements may jopanetize the validity of the application or any	ents made on information and belief are believed to be true; and to made are punishable by fine or imprisonment, or both, under 18 patent issued thereon.
0)	SOLE OR FIRST INVENTOR	Citizenship
- (1	Given Name (first and Middle (if any)) Luc	French Family Name or Surmanne AUJAME
199	Full Mailing Address 477, Chemin du Puits - 69210 FLEURIEUX SUR L'	
lan.	Residence - City, State/Country (if different from PO address) same as above	ADREDDE - TRANCE 1 1/2
	SIGN AND DATE HERE Inventor's Signature	Date 9-7.2001
	SECOND JOINTINVENTOR	1,000
	(if any)	Ciuzenship French Franiy Name
- 00	Given Name (first and Middle [if any]) Annabelle	or Surname BOUCHARDON
	Full Mailing Address 7, rue Nicolai - 69007 LYON - FRANCE FIR X Residence Cuty State Country (different from PO address) same as above)
	SIGN AND DATE HERE Inventor's Signature	Date 31.7.2001
	THIRD JOINT INVENTOR (if any)	Citizenship
_	Given Name (first and Middle [if any]) Geneviève	Front Family Name of Surname RENAULD-MONGENTE
	Residence - City, State/Country	TRANCE / 102
	(if different from PO address) same as above SIGN AND DATE HERE Inventor's Signature G. Ren and o	Date 10.07.2001
	FOURTH JOINTINVENTOR	Citizenship
	(if any)	French Family Name
. 00	Given Name (first and Middle [if any]) Bachra	or Surname ROKBI
	Full Mailing Address 254, rue Vendôme - 69003 LYON - FRANCE	× .
	Residence - City, State/Country (if different from PO address) same as above /	
	SIGN AND DATE HERE Inventor's Signature	Date 11.07.2001
	LARSON & TAYLOR, PLC • 1199 North Fairfax Street • Suite 96	00 • Alexandria Virginia 22314 11/98

DECLARATION FOR USA PATENT APPLICATION

(including Design and National Stage PCT)

ADDITIONAL INFORMATION SHEET (use as required)

U.S. Provisional Application No.	pited States PROVISIONAL a Parent Filing Date	(Day/Month/Year)	
Additional Prior Foreign Application(s)		•	
Prior Foreign Application No.	Country	Day/Month/Year Filed	Priority <u>Not</u> Claimed
Additional 35 U.S.C. § 120 application(s)			
U.S. or PCT Parent Application No.	Parent Filing Da	ate (Day/Month/Year) Parent P.	atent No. (if applicable)
		and the second s	, .
Additional Joint Inventor(s):	ENTOR	Citizenship	
Given Name (tirst and Middle [if any]) Xavier		French Family Name or Surname NASSI	F
Full Mailing 1, Square Charles Laure	ent- 75015 <u>PARIS</u>	- FRANCE FT≥×	
Residence - City, State/Country (if different from PO address) same, as about SIGN AND DATE HERE Inventor's Signature	ve	Date 20 Yuu	2001
SIXTH JOINT IN	ENTOR	Citizenship	
Given Name (first and Middle [if any]) Colin		British Family Name or Sumame TINSLE	2Y
and Middle [if any]) Colin Full Mailing Address 16, Square Jean Thébau	ıd - 75015 PARIS		
Residence - City, State/Country (if different from PO address) same as above	ve		
SIGN AND DATE HERE Inventor's Signature	insley	Date 7 juin 2	2001
SEVENTH JOINT II (if any)	VENTOR	Citizenship	
Given Name (first and Middle [if any]) Agnès	200	French Family Name or Surname PERR	RIN
Full Mailing 33 bis, rue du Docteur	r Roux - 75015 <u>P</u>		
Residence - City, State/Country (if different from PO address) same as about	e		
SIGN AND DATE HERE Inventor's Signature		Date 19 ju	u 2001
EIGHTH JOINT IN (if any)	IVENTOR	Citizenship	
Given Name (first and Middle [if any])		Family Name or Sumame	
Full Mailing Address			
Residence - City, State/Country (if different from PO address) SIGN AND			
DATE HERE Inventor's Signature		Date	

•

PCT/FR99/02643

SEQUENCE LISTING

- <110> Pasteur Mérieux Sérums et Vaccins
 INSERM
- <120> Nucleic acids and polypeptides specific for the pathogenic strains of the Neisseria genus
- <130> BET 99/0918

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		22	.5				12	0				12	5		u Pro	
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Pro Gln Gln Pro Leu Thr Ser Tyr Phe Gln Ala Ala Leu Thr Ala Leu 145 $$150\$

Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln 165 $$170\$

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Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala \$260\$

Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile 275 \$280\$

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Pro Lys Lys Thr Ala Trp Glu Pro Asp Glu Ile Ile Trp Lys Lys Val 305 310 320

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att Ile	cac His	aco Thi	tt:	999 1 Gl ₃ 485	Ty:	gat Asp	ato Met	ecg Pro	ggtt Val	. Se	ggt Gly	tgt / Cys	cgc Arg	gaa Glu 499	ggc Gly	1488
t C g	gta Val	ac ₉ Thr	Gly 500	aac Asn	Leu	g att	acq Thr	Gly SOS	gat Asp	ge: Ala	Gly Gly	Ser	Leu : 510	aac Asn	att Ile	1536
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<213> Neisseria meningitidis

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Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala 35 \$40\$

Phe Phe Ala Phe Ser Ile Ile Ala Asn Asn Val His Tyr Ala Val Tyr 65 75

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Ile 85 90 95

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu 100 105 110

Pro Ala Leu Trp Gly Vai Leu Glu Val Met Leu Phe Cys Ser Leu Ala 115 120 125

Lys Phe His Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe 130 135 140

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His 145 155 160

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe 165 170 175

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp 180 \$180\$

Leu Ser Arg Ile Pro Ala Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly
195 200 205

Gln Gly Ser Val Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser 210 . 215 220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 \$230\$

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn Ala Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 280 Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 295 Ser Ala Gln Ala Glu Asn Glu Met Ala Ile Leu Asn Leu Ile Gly Lys 310 Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn Gly Asp Asn Met Pro Asp Glu Lys Leu Deu Pro Leu Phe Asp Lys Ile Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 360 His Ala Pro Tyr Ser Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly Glu Leu Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Leu Val Pro Leu

Val Leu Tyr Ser Ser Asn Lys Ala Val Gln Gln Ala Ala Asn Gln Ala 450 455 460 460 460 460 460 460 460 470 460 475 480 460 475 480

Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu Gly

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Ctg	tco Ser	tai Ty:	c Tys	gto Val	cgt L Arg	cgc Arg	ggc G1 ₂ 680	/ Asr	gcg Ala	g gca L Ala	a cgg	act Thr 685	- Ala	tcg a Sei	g gca : Ala	2064
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		c ggt ctg a Gly Leu 1030	Gly Ala					3120
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- Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp 165 170 175
- Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
- Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
- His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly 210 215 220
- Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn 225 230235235
- Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn 245 250 255
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- Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala 275 280 285
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- Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly 305 $$310\$
- Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser
- Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro \$340\$
- Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val 355 360 365
- Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr $_{370}$
- Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr 385 390 395 400
- Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile 405 410 415
- Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser 420 425 430

Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly 435 440 445

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Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala 465 \$470\$

Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile 485 490 495

Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu 500 505 510

His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser 515 520 525

Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys 530 540

Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser 545 550555 555 560

Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu $_{\rm 565}$ $_{\rm 570}$

Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu 580 585 590

Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Cly Thr Ala Met Thr 595 600 605

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Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly 625 630 635 640

Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu $_{645}$ $_{650}$ $_{650}$

Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr $_{660}$

Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala 675 680 685

Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly 690 695 700

Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser . 705 710715715

Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp $725 \\ 730 \\ 735$

Met Pro Gly Ile Arg Pro Tyr Gly Ála Thr Phe Arg Ala Ala Ala Ala 740 745 750

- Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu $755 \hspace{1.5cm} 760 \hspace{1.5cm} 765 \hspace{1.5cm}$
- Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gl
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- Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr 785 790 795 800
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- Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly 820 825 830
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- Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp 850 860
- Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly 865 870 875 880
- Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser 885 890 895
- Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr 900 905 910
- Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala 915 920 925
- Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys 930 935 940
- Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn 945 950 955 960
- Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser 965 970 975
- Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu 980 985 990
- Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly 995 1000 1005
- Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr 1010 1015 1020
- Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp 025 1030 1035
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  Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
  cag gaa cgt gee geg ttt gee ttg gge gte age caa aat gee gta aaa
                                                                  144
  Gin Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gin Asn Ala Val Lys
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  atc age aac ege age aat gaa age ata ege atc aac tit acc gea act
  Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
  gtg ggt aag cgc gtg agc caa tgc tat gtt acc agt gta atc agc aca
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  Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr
  65
  atc ggc gtt acc act tee gat gea att tgt ttg gga ggc gga acg cac
                                                                  288
  Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His
                  85
  aaa ggc aaa agt caa tgc aat gct ttg ctt aaa gcg gca ggc cgt tgc
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 Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys
  taa
                                                                  339
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 . Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
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Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys 25 40 . 45 Lle Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr

Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr 65 70 75 80

Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His $90\,$ 95

Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys 100 105 110

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ctg ctg acg gaa aaa gtg tcg ccc atc atc gca tta atc ttg gtg ccg 96 Leu Leu Thr Glu Lys Val Ser Pro Tie Tie Ala Leu Tie Leu Val Pro 20 25 30

ctg ttt ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa 144 Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu 35 40 45

tot tat tog ggc ggc acc aca tog gtg atg cag att gtg att atg ttt 192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe
50 60 60

atg tit too att tig tit tit gga atc atg aac gat gig ggg cig tit. 240 Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe Gly Ile Met Asn Asp Val Gly Leu Phe Gly Ile Met Asn Asp Val Gly Leu Phe Gly Ile Met Asn

cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg 288 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val

gca gtg agt gtg ggg acg gtc ttg gtg tcg gtg gtg gcg cag ttg gac 336 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp

ggg gcg ggt gcg acg acg ttt tta ttg gtc gtc ccc gcc ctt ttg ccg 384 Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro Ala Leu Leu Pro 120

ctt tac aag egt etg cat atg aat oct tac etg etg tit ittg etg etg 432 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu 130 135 140

act too agt gog gga ttg att aac oft otg cog tgg ggc ggg cog acc 480

Thr 145	Ser	Ser	Ala	Gly	Leu 150	Ile	Asn	Leu	Leu	Pro 155	Trp	Gly	Gly	Pro	Thr 160	
Gly 999	cgg Arg	gtt Val	gca Ala	agc Ser 165	gtg Val	ttg Leu	ggc Gly	gca Ala	gat Asp 170	gtg Val	ggc Gly	gaa Glu	ttg Leu	tat Tyr 175	aaa Lys	528
cct Pro	ttg Leu	ttg Leu	acg Thr 180	gtg Val	caa Gln	att Ile	atc Ile	ggt Gly 185	gtg Val	gtg Val	ttt Phe	atc Ile	ctt Leu 190	gcg Ala	ctg Leu	576
tcc Ser	ctg Leu	ctt Leu 195	ttg Leu	ggt Gly	gtg Val	cgt Arg	gaa Glu 200	aaa Lys	agg Arg	cgg Arg	att Ile	gtc Val 205	cgg Arg	gag Glu	ttg Leu	624
ggc Gly	gcg Ala 210	ttg Leu	ecc Pro	gcc Ala	gtg Val	gcg Ala 215	gat Asp	ttg Leu	ata Ile	aag Lys	ccg Pro 220	gtg Val	ect Pro	ttg Leu	ecg Ser	672
gaa Glu 225	gaa Glu	gaa Glu	caa Gln	aaa Lys	ttg Leu 230	gcg Ala	cgt Arg	ecg Pro	aaa Lys	ctg Leu 235	ttt Phe	tgg Trp	tgg Trp	aat Asn	gtc Val 240	720
ctg Leu	ctg Leu	ttt Phe	ttg Leu	gcg Ala 245	gcg	atg Met	agc Ser	ctg Leu	ctt Leu 250	ttt Phe	tog Ser	Gly Gly	atc Ile	ttc Phe 255	ccg Pro	768
ccg Pro	ggt Gly	tat Tyr	gta Val 260	tt: Phe	atg Met	ctg Leu	gct Ala	gca Ala 265	acg Thr	gcg Ala	gcg Ala	ttg Leu	ctt Leu 270	ttg Leu	aat Asn	816
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ggc Gly	gcg Ala 290	gtg Val	atg Met	atg Met	geg Ala	tee Ser 295	att Ile	att Ile	ttg Leu	gcg Ala	gca Ala 300	gg: Gly	acg Thr	ttt Phe	ttg Leu	912
999 Gly 305	att Ile	ttg Leu	aag Lys	ggt Gly	gcg Ala 310	ggg Gly	atg Met	ttg Leu	gac Asp	gcg Ala 315	att Ile	tcc Ser	aaa Lys	gac Asp	att Ile 320	960
gtg Val	cat His	atc Ile	ctg Leu	ccg Pro 325	gac Asp	gcg Ala	ctg Leu	ctg Leu	cct Pro 330	tat Tyr	ctg Leu	cat His	att Ile	gcc Ala 335	atc Ile	1008
ggt Gly	gtg Val	ttg Leu	ggc Gly 340	att Ile	ccg Pro	ctt Leu	gag Glu	ttg Leu 345	gtt Val	ttg Leu	agt Ser	acg Thr	gac Asp 350	gct Ala	tat Tyr	1056
tat Tyr	Phe	gga Gly 355	ctg Leu	ttt Phe	ccg Pro	att Ile	gtg Val 360	gag Glu	cag Gln	att Ile	acc Thr	tcg Ser 365	cag Gln	gcg Ala	ggc Gly	1104
gtg Val	gcg Ala 370	ccc Pro	gaa Glu	gca Ala	gca Ala	ggt Gly 375	tat Tyr	gcg Ala	atg Met	ttg Leu	atc Ile 380	ggc Gly	agt Ser	atc Ile	gtc Val	1152
ggc	act	ttt	gtt	acg	ccg	ctt	tcg	ccg	gct	ttg	tgg	atg	ggc	ttg	ggt	1200

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 395 390 395 400

ttg gog aaa ttg tog atg ggc aaa cac ato cgt tat tog ttt ttt tgg 1248
Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp 405 415

gog tgg ggt ttg tog otg gog ata ttg goc agt tog ata gog goa gga Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly 420 430

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1114

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<213> Neisseria meningitidis

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- Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser 210 215 220
- Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val 225 230 235 240
- Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
- Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Asn $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$
- Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly 275 280 285
- Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu 290 295 300
- Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile 305 310 315
- Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
- 325 330 335
 Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
- 340 345 350

 Tyr Phe Gly Leu Phe Pro Ile Val Glu Glr. Ile Thr Ser Gin Ala Gly
- 355 360 365 Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
- 370 375 380
- Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 385 390 195
- Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp \$405\$
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1	•			5			,		10		2-			15		
act Thr	tat Tyr	ctg Leu	tat Tyr 20	caa Gln	aag Lys	ccc Pro	aag Lys	ctc Leu 25	ttt Phe	aaa Lys	gga Gly	gcg Ala	gtt Val 30	cgg Arg	aat Asn	96
ctc Leu	gaa Glu	gcc Ala 35	gca Ala	tot Ser	tgt Cys	aaa Lys	tat Tyr 40	atc Ile	aac Asn	gag Glu	ata Ile	tac Tyr 45	caa Gln	cga Arg	gca Ala	144
gac Asp	cca Pro 50	acc Thr	gca Ala	ccg Pro	ctg Leu	ttt Phe 55	cat His	ctg Leu	cgt Arg	aaa Lys	aaa Lys 60	ggc Gly	gca Ala	atc Ile	gtt Val	193
ect Pro 65	aaa Lys	gaa Glu	gaa Glu	tac Tyr	gtc Val 70	gaa Glu	agt Ser	ttc Phe	gac Asp	gat Asp 75	ttg Leu	ggc Gly	aaa Lys	act Thr	ege Arg 80	24
tac Tyr	cgt Arg	ttt Phe	att Ile	aaa Lys 85	tcc Ser	gtt Val	atc Ile	tac Tyr	gaa Glu 90	cat His	atg Met	aag Lys	aat Asn	ggt Gly 95	gcg Ala	28
			tat Tyr 100													33
gcc Ala	cgt Arg	caa Gln 115	gtc Val	gcc Ala	cgc Arg	ttt Phe	gcc Ala 120	ggc Gly	gca Ala	cat His	act Thr	att Ile 125	gtt Val	agt Ser	gga Gly	38
tat Tyr	Leu 130	Ala	ttt Phe	ggc Gly	agc Ser	gac Asp 135	gaa Glu	tct Ser	tat Tyr	aaa Lys	aac Asn 140	cat His	tgg Trp	gat Asp	acc Thr	43
cgc Arg 145	Asp	gtg Val	tat Tyr	gcc Ala	atc Ile 150	cag Gln	ctt Leu	ttc Phe	ggc Gly	aag Lys 155	aaa Lys	cgt Arg	tgg Trp	caa Gln	ctt Leu 160	48
act Thr	gco	cct Pro	gat Asp	ttc Phe 165	Pro	atg Met	cca Pro	ttg Leu	tat Tyr 170	atg Met	caa Gln	cag Gln	act Thr	aaa Lys 175	gat Asp	52
act Thr	gat	att Ile	Ser 180	Ile	cct Pro	gaa Glu	cat His	atc Ile 185	Asp	atg Met	gat Asp	att Ile	atc Ile 190	ctt Leu	gaa Glu	57
			gtc Val					Arg								62
ccg	Let 210	Gly	tgt Cys	gaa Glu	acc Thr	ttc Phe 215	cac	ttc Phe	gct Ala	gtc Val	ggt Gly 220	Thr	ttc Phe	ccg Pro	ccc Pro	67
aac Asn 225	Gly	tat Tyr	aat Asn	tac Tyr	Leu 230	Glu	tgg	cta Leu	atg Met	aag Lys 235	Lys	ttc Phe	Pro	acg	ata 11e 240	73
gaa Glu	agt Ser	cto Lev	g cgc	His	agt Ser	ttc Phe	tca Ser	gac Asp	tgg	gag Glu	caa Gln	gat Asp	agg Arg	acg	cgt Arg	7

	245	25	10	255
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aat tac gaa gcc Asn Tyr Glu Ala 275	ttc agt gaa Phe Ser Glu	gac ttc ct Asp Phe Le 280	c ggc aaa gaa u Gly Lys Glu 285	ege ace gat 864 Arg Thr Asp
acc gct ttt cat Thr Ala Phe His 290	ctc gaa cag Leu Glu Glr 295	Phe Ala As	at eee aae get sn Pro Asn Ala 300	act ccg ctt 912 Thr Pro Leu
tca gac gac gto Ser Asp Asp Val 305	agg tig aga L Arg Leu Arg . 310	a cta aat go g Leu Asn Al	c aat aat ttg La Asn Asn Leu 315	gat acg ttg 960 Asp Thr Leu 320
gas aag gga ta Glu Lys Gly Ty:	tig att ggg Leu Ile Gly 325	g aat ggg at / Asn Gly Me 33	et Lys Ile Ser	gta gat gaa 1008 Val Asp Glu 335
ttg ggg aaa aaa Leu Gly Lys Ly: 34	s Val Leu Glu	a cac atc gg i His Ile Gl 345	gt aag aat gaa ly Lys Asn Glu	ccg tta ttg 1056 Pro Leu Leu 350
tig aaa aat ci Leu Lys Asn Le 355	a cig gtt aad u Leu Val Asi	tto aat ca n Phe Asn Gl 360	ag gga aaa cat ln Gly Lys His 365	gaa gaa gtt 1104 Glu Glu Val
agg aag ttg at Arg Lys Leu Il 370	t tat cag tto e Tyr Gln Leo 37	u Ile Glu Le	ta gat tit ctg eu Asp Phe Leu 380	gaa ctt ttg 1152 Glu Leu Leu
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1 Thr Tyr Leu Ty	5			15
1 Thr Tyr Leu Ty	5 yr Gln Lys P 20	ro Lys Leu 25	10 Phe Lys Gly Al Asn Glu Ile Ty	15 La Val Arg Asn 30
Thr Tyr Leu Tyr Leu Glu Ala A: 35	5 yr Gln Lys P 20 la Ser Cys L la Pro Leu P	ro Lys Leu 25 ys Tyr Ile 40	10 Phe Lys Gly Al Asn Glu Ile Ty	15 Ia Val Arg Asn 30 /r Gln Arg Ala
Thr Tyr Leu Ty Leu Glu Ala As 35 Asp Pro Thr A 50 Pro Lys Glu G 65	5 Yr Gln Lys P 20 La Ser Cys L La Pro Leu P Lu Tyr Val G 70	ro Lys Leu 25 ys Tyr Ile 40 he His Leu 55 lu Ser Phe	Dhe Lys Gly Al Asn Glu Ile Ty Arg Lys Lys G 60 Asp Asp Leu G	15 Ia Val Arg Asn 30 /r Gln Arg Ala

CIBUCALD DOLDCA

- Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile 100 105 110
- Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly 115 120 125
- Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr 130 140
- Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu 145 150 155 160
- Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp \$155\$
- Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu 180 185 190
- Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile 195 \$200\$
- Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro 210 220
- Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile 225 \$230\$
- Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg 245 \$250\$
- Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val\$260\$
- Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp 275 280 285
- Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu 290 295 300
- Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu 305 \$310\$
- Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu \$325\$
- Leu Gly Lys Lys Val Leu Glu Hıs Ile Gly Lys Asn Glu Pro Leu Leu 340 345 350
- Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val 355 360 365
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ttt Phe	tcc Ser	cta Leu 35	tgg Trp	acg Thr	aca Thr	ttt Phe	gca Ala 40	tcg Ser	ata Ile	tct Ser	gcg Ala	tta Leu 45	ttg Leu	att Ile	atc Ile	144
			ata Ile													192
caa Gln 65	Ile	tta Leu	cct Pro	gca Ala	tcg Ser 70	ggc Gly	gta Val	atc Tle	agg Arg	gtg Val 75	tat Tyr	gca Ala	ccg Pro	gat Asp	acg Thr 80	240
			aca Thr													288
ggc Gly	gac	aag Lys	cta Leu 100	Phe	gcg Ala	ctt Leu	tog Ser	acc Thr 105	tca Ser	egt Arg	ttc Phe	ggc	gca Ala 110	gga Gly	gat Asp	336
agc Ser	gtg	Cag Gln 115	cag Gln	cag Gln	ttg Leu	aaa Lys	acg Thr 120	gag Glu	gca Ala	gtt Val	ttg Leu	aag Lys 125	aaa Lys	acg Thr	ttg Leu	384
gca Ala	gaa Glu 130	Gln	gaa Glu	ctg Leu	ggt Gly	cgt Arg 135	ctg Leu	aag Lys	ctg Leu	ata Ile	cac His 140	ejà aaa	aat Asn	gaa Glu	acg Thr	432
	Ser		aaa Lys			Val					Asn					480
			cag Gln		Asp					Arg						528
gaa Glu	atg 1 Met	ttg Leu	Cag Gln 180	Lys	tat Tyr	egt Arg	ttc Phe	cta Leu 185	Ser	gcc	aat Asn	gat Asp	gca Ala 190	Val	cca Pro	576
aaa Lys	caa Glr	gaa Glu 199	atg Met	atg Met	aat Asn	gtc Val	aag Lys 200	Ala	gag Glu	Leu	tta Leu	gag Glu 205	Gln	aaa Lys	gcc Ala	624
												Leu			atc ı Ile	672
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<213> Neisseria meningitidis

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Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly 50 55 60

Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr $65 70 70$

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala 85 90 95

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp 100 $$105\$

Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu 115 \$120\$

Ala Glu Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr 130 \$135\$

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His 145 155 160

Ile Ser Gln Gln Ele Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala 195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile 210 . 215 220

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<213> Neisseria meningitidis

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  Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gin Glu Ile Arg Thr Gln
  aat otg aca ttg goo ago oto ooc aaa ogg cat gag aca gaa caa ago
  Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 cag ctt gaa ege ace atg gee gat att tet caa gaa gtt ttg gat ttt
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
  gaa atg cgc tot gaa caa atc atc cgt gca gga cgg tcg ggt tat ata
  Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
  goa ata cog aac gto gaa gto gga cag cag gtt gat cot too aaa ctg
  Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu
  ctc ttg ago att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat
  Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
                                  105
  atc ccc age agt goa goa gge tit atc aag ccg aaa gac aag git gtc
  Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
  cta egt tat cag goa tat coc tat caa aaa tte ggg ett get tee gge
  Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
      130
  agt gtc gta tca gta gca aaa acg gca ctg ggc aga cag gaa ttg tcg
  Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
  145
                      150
                                           155
   gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt
                                                                     52B
  Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
   tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt
  Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
                                   185
   gag gaa aaa ccg ctg caa atc ggc atg acg ttg gaa gca gac atc ctg
  Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
                               200
  cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ctg att tat agt
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215

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<213> Neisseria meningitidis

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As n Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser 35 40 45

Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe 50 60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile 65 70 75 80

Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu 85 90 95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr 100 105 110

Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val 115 120 125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly 130 135 140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser 145 150 155

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val 165 170 175

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly 180 185 190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu 195 200 205

His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser 210 215 220

Met Ser Gly Lys Leu 225

<210> 19

<211> 1743

<212> DNA

<213> Neisseria meningitidis

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ggc	ttg Leu	gaa Glu 195	aac Asn	ctg Leu	egt Arg	cgt Arg	ttg Leu 200	ecg Pro	agt Ser	gtt Val	aaa Lys	aca Thr 205	gat Asp	att Ile	cag Gln	624
att Ile	ata Ile 210	ccg Pro	tcc Ser	gaa Glu	ga a Glu	gaa Glu 215	ggc Gly	aaa Lys	agc Ser	gat Asp	tta Leu 220	cag Gln	atc Ile	aaa Lys	tgg Trp	672
cag Gln 225	cag Gln	aat Asn	aaa Lys	ccc Pro	ata Ile 230	cgg Arg	ttc Phe	agt Ser	atc Ile	ggt Gly 235	ata Ile	gat Asp	gat Asp	gcg Ala	ggc Gly 240	720
ggc Gly	aaa Lys	acg Thr	acc Thr	ggc Gly 245	aaa Lys	tat Tyr	caa Gln	gga Gly	aat Asn 250	gtc Val	gct Ala	tta Leu	tcg Ser	tcc Ser 255	gat Asp	768
aac Asn	cct Pro	ttg Leu	99c Gly 260	tta Leu	agc Ser	gat Asp	tcg Ser	ttt Phe 265	tat Tyr	gtt Val	tca Ser	tat Tyr	gga Gly 270	cgc Arg	ggt Gly	816
ttg Leu	gtg Val	cac His	aaa Lys	acg Thr	gac Asp	ttg Leu	act Thr 280	gct Ala	gcc Ala	acc Thr	ggt Gly	acg Thr 285	gaa Glu	act Thr	gaa Glu	864
agc Ser	gga Gly 290	Ser	aga Arg	agt Ser	tac Tyr	agc Ser 295	gtg Val	cat His	tat	teg	gtg Val 300	ecc Pro	gta Val	aaa Lys	aaa Lys	912
Igg Trp 305	Leu	ttt Phe	tet	ttt Phe	aat Asn 310	cac	aat Asn	gga Gly	cat	cgt Arg 315	Tyr	cac His	gaa Glu	gca Ala	acc Thr 320	960
gaa Glu	ggo Gly	tat Tyr	Ser	gtc Val	Asn	tac Tyr	gat Asp	tac Tyr	aac Asr 330	Gly	aaa Lys	caa Gln	tat Tyr	cag Gln 335	agc Ser	1008
ago	cto Lev	gcc Ala	gco Ala 340	Glu	ogo Arg	atg Met	ctt Leu	tgg Trp 345	Pro	Pro	ago Ser	ttt Phe	pro 350	GIL	act	1056
t Ca	gto Val	cga L Arg 355	Met	aaa Lys	tta Lev	tgg	aca Thr	Arg	caa Gl:	a acc	tat Tyr	Lys 365	Tyr	ato Ile	gac Asp	1104
gat	gc Ala 37	a Glu	ato Ile	gaa EGlu	gtg Val	Glr 375	n Arg	cgo Arg	cg Ar	g Ser	gca Ala 380	a Gly	tgg Trp	gaa Glu	gcc 1 Ala	1152
gaa Glu 385	ı Le	g ogo	Cac Hi	e egt	got Ala	ту:	c cto	cac His	cg Ar	t tgg g Trp 399	p Gli	g ctt	gac LAsp	gg Gly	aag / Lys 400	1200
tt: Le:	g to 1 Se	t tac r Ty	aa: Ly	a cge s Are	g Gl	g aco	c ggd r Gl	e ato	g cg : Ar 41	g Gl	a ag n Se	t ato	g ccc	gc Al:	a cct a Pro 5	1248
ga	a ga	a aa	gg s	c gg	gg g	c ac	t at	t cc	a gc	c ac	a tc	c cg	t at	g aa	a atc	1296

	Glu	Glu	Asn	Gly 420	Gly	Gly	Thr	Ile	Pro 425	Ala	Thr	Ser	Arg	Met 430	Lys	Ile		
	ata Ile	acc Thr	gcc Ala 435	gga Gly	ttg Leu	gat Asp	gca Ala	gcg Ala 440	gcc Ala	ccg Pro	tot Ser	atg Met	ttg Leu 445	ggc	aaa Lys	cag Gln		1344
									caa Gln									1392
	ttg Leu 465	gtt Val	gcc Ala	caa Gln	gac Asp	aag Lys 470	ttg Leu	tet Ser	atc Ile	ggc Gly	agc Ser 475	cgc Arg	tac Tyr	acc Thr	gtt Val	cgc Arg 480		1440
	gga Gly	ttt Phe	gat Asp	999 999	gag Glu 485	cag Gln	agt Ser	ctt Leu	ttc Phe	gga Gly 490	gag Glu	cga Arg	ggc Gly	tto Phe	tac Tyr 495	tgg Trp		1488
									cat Kis 505									1536
									ggc Gly									1584
	ggc Gly	aag Lys 530	Gln	ctg Leu	atg Met	ggt Gly	gca Ala 535	Val	gtc Val	ggc Gly	ttc Phe	aga Arg 540	gga Gly	999 Gly	cat His	aaa Lys		1632
	gta Val 545	ggc Gly	ggt Gly	atg Met	ttt Phe	gct Ala 550	tat Tyr	gat Asp	ctg Leu	ttt Phe	gcc Ala 555	gge Gly	aag Lys	eeg Pro	ctt Leu	cat His 560		1680
	aaa Lys	ccc	aaa Lys	ggc Gly	ttt Phe 565	Gln	acg	acc	aac Asn	acc Thr 570	gtt Val	tac Tyr	ggc Gly	ttc Phe	aac Asn 575	ttg		1728
	ast Asn	tac Tyr	agt Ser	ttc Phe 580	taa													1743
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< 2	211:	> !	580															
< 2	212:	> :	PRT															
<2	213:	> 1	Nei	sse	ria	. me	nir	ngit	idí	s								
				e Pi	ie P	ro A	la 1	Pro	Cys	Leu	Leu 10	Val	114	e Le	u Al		al 15	Ile
	Pro	Lei	u Ly		r L	éu A	la i	Ala.	Asp	Glu 25	Asn	Asp	Ala	e Gl		u I	le	Arg
	Ser	Me:		n Ai	g G	ln G	ln 1	His	Ile 40	Asp	Ala	Glu	Le		u Tl	ır A	sp	Ala
	Asn	. Va	l Ar	g Pl	ne G	lu G	ln :	Pro	Leu	Glu	Lys	Asr	As	п Ту	r Va	al L	eu	Ser

	50					55					60				
Glu 65	Asp	Glu	Thr	Pro	Cys 70	Thr	Arg	Val	Asn	Tyr 75	Ile	Ser	Leu .	Asp.	Asp 80
Lys	Thr	Ala	Arg	Lys 85	Phe	Ser	Phe	Leu	Pro 90	Ser	Val	Leu	Met	Lys 95	Glu
Thr	Ala	Phe	Lys 100	Thr	Gly	Met	Cys	Leu 105	Gly	Ser	Asn	Asn	Leu 110	Ser	Arg
Leu	Gln	Lys 115	Ala	Ala	Gln	Gln	11e 120	Leu	Ile	Val	Arg	Gly 125	Tyr	Leu	Thr
Ser	Gln 130	Ala	Ile	lle	Gln	Pro 135	Gln	Asn	Met	Asp	Ser 140	Gly	Ile	Leu	Lys
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Arg	Asp	Ala	Lys	Ser 165	Ala	Glu	Gly	Ser	Ile 170	Ser	Ala	Phe	Asn	Asn 175	Lys
Leu	Pro	Leu	Tyr 180	Arg	Asn	Lys	Ile	Leu 185	Asn	Leu	Arg	Asp	Val 190	Glu	Gln
Gly	Leu	Glu 195	Asn	Leu	Arg	Arg	Leu 200	Pro	Ser	Val	Lys	Thr 205	Asp	Ile	Gln
Ile	1le 210		Ser	Glu	Glu	Glu 215	Gly	Lys	Ser	Asp	Leu 220	Gln	Ile	Lys	Trp
Glr 225		Asr	. Lys	Pro	Ile 230	Arg	Phe	Ser	Ile	Gly 235	Ile	Asp	gsA	Ala	Gly 240
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Asr	Pro	Let	1 Gly 260		Ser	Asp	Ser	Phe 265	туг	· Val	Ser	Tyr	Gly 270	Arg	Gly
Let	ı Val	His 275		Thr	Asp	Let	1 Thr 280		ı Ala	a The	c Gly	7 Thr 289	r Glu	Thr	Glu
Set	29		r Arg	g Ser	Tyr	Se:		L His	s Ty:	s Se	r Val	L Pro	o Val	Lys	Lys
Tr:		ı Ph	e Ser	Phe	310		s Ası	n Gl	/ Hi	s Ar	g Ty:	r His	s Glu	a Ala	320
Gl	u Gl	у Ту	r Se	c Val		Ty:	r As	р Ту:	r As:	n Gl	y Ly:	s Gli	n Ty	Glr 335	Ser
Se	r Le	u Al	a Ala		ı Arş	g Me	t Le	u Tr	p Pr	o Pr	o Se	r Ph	e Pro	Glr	1 Thr

375

Glu Leu Arg His Arg Ala Tyr Leu His Arg Trp Gln Leu Asp Gly Lys 390

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro

Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile

Ile Thr Ala Gly Leu Asp Ala Ala Pro Ser Met Leu Gly Lys Gln

Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro

Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg 465

Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp

Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu 505

Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser

Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys

Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His

Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu

Asn Tyr Ser Phe

<210> 21

370

<211> 411

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

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gaa Glu	gcg Ala	aaa Lys 35	caa Gln	acc Thr	gcc Ala	ctg Leu	att Ile 40	gcc Ala	acc Thr	tat Tyr	cgg Arg	cat His 45	tct Ser	tct Ser	atg Met	144
gtt Val	gcg Ala 50	gcg Ala	gaa Glu	caa Gln	tac Tyr	gcc Ala 55	ttg Leu	cag Gln	ctt Leu	aaa Lys	aaa Lys 60	gcg Ala	cag Gln	gac Asp	gaa Glu	192
agg Arg 65	cag Gln	egg Arg	tgg Trp	tac Tyr	gac Asp 70	ttt Phe	tcc Ser	caa Gln	aaa Lys	caa Gln 75	gga Gly	aga Arg	aag Lys	ccc Pro	gtg Val 80	240
aaa Lys	aaa Lys	cag Gln	tat Tyr	ecg Pro 85	ccg Pro	caa Gln	acg Thr	aaa Lys	aaa Lys 90	gcc Ala	ggc	tat Tyr	ctg Leu	aaa Lys 95	acc Thr	288
aag Lys	gaa Glu	gaa Glu	ctg Leu 100	ctt Leu	gcg Ala	gaa Glu	ttg Leu	gct Ala 105	tgc Cys	ctt Leu	aaa Lys	gcg Ala	gaa Glu 110	atg Met	gct Ala	336
gcc Ala	cta Leu	aaa Lys 115	Lys	ctc Leu	gat Asp	gcc Ala	tta Leu 120	atc	tat Tyr	ggg Gly	aaa Lys	gaa Glu 125	gtg Val	cgg Arg	cag Gln	384
		Arg			tcg Ser			taa								411

<210> 22

<211> 136

<212> PRT

<213> Neisseria meningitidis

<400> 22
Met Ile Glu Phe Val Arg Ala Lys Lys Arg Leu Leu Trp Ala Phe Val

Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala $20 \ 25 \ 30$

Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met $35 \ \ 40 \ \ 45$

Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu 50 $\,$ 55 $\,$ 60 $\,$

Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val 65 70 75 80

Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr $85 \ 90 \ 95$

Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala 100 105 110

Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln 115 120 ' 125

Lys Glu Arg Asn Ser Ser Gln Gly

<210> 23

<211> 924

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(921)

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												atc Ile				192
												tgg Trp				240
												ttg Leu				288
												gcg Ala				336
aaa Lys	tta Leu	ctt Leu 115	tct Ser	tcc Ser	ggc	aaa Lys	cgc Arg 120	tgt Cys	ttg Leu	agt Ser	ttg Leu	ggc Gly 125	ggc Gly	gac Asp	cat His	384
ttc Phe	att Ile 130	acc Thr	ctc Leu	ccg Pro	ttg Leu	ttg Leu 135	cgc Arg	gcc Ala	cac His	gcc Ala	cgc Arg 140	tat Tyr	ttc Phe	ggc Gly	aaa Lys	432
ctc Leu 145	gca Ala	ctg Leu	att Ile	cat His	ttt Phe 150	gac Asp	gcg Ala	cac His	acc Thr	gac Asp 155	acc Thr	tac Tyr	gac Asp	aac Asn	ggc Gly 160	480
												ccc Pro				528
ctc	atc	gac	ccg	tcc	cgt	tcc	gta	caa	atc	ggc	ata	cgt	acc	gaa	cac	576

Leu	Ile	Asp	Pro	Ser	Arg	Ser	yal	Gln 185		Gly	Ile	Arg	Thr	Glu	His	
agt Ser	aaa Lys	aaa Lys 195	ttg	cct Pro	ttt Phe	act Thr	Val	ttg Leu	acc Thr	gcc Ala	ccc Pro	caa Gln 205	gtt Val	aat Asn	gaa Glu	624
gac Asp	Ser	gtt Val	gaa Glu	gag Glu	acc Thr	Val	cgt Arg	aaa Lys	atc Ile	aaa Lys	Glu	acc	gtc Val	ggc Gly	aat Asn	672
		gtt Val														720
225		999			230					235					240	768
Ala	Pro	Gly	Thr	Gly 245	Thr	Pro	Val	Cys	Gly 250	Gly	Leu	Ser	Ser	Asp 255	Arg	700
gca Ala	tta Leu	aaa Lys	atc Ile 260	cta Leu	ogt Arg	999 Gly	ctg Leu	acg Thr 265	Asp	ctc Leu	gac	atc Ile	gtc Val 270	ggt Gly	atg Met	816
		gta Val 275														864
		Gly														912
	Lys	gac Asp	tga													924
<210	>	24														
<211	>	307														
<212	>	PRT														
<213	> :	Nei	ssei	ria	mer	ning	git:	idi	3							
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1				5						10	-				15	
Asn	Asn	Phe	Gly 20		Le	u Ar	g L	eu P	ro 1 25	Leu	Asn	Phe	Met	Pro 30	Tyr	Glu
Ser	His	Ala 35	Asp	Trp	Va	1 11		hr G 40	ly '	Val	Pro	Tyr	Asp 45	Met	Ala	Val
Ser	Gly 50	Arg	Ser	Gly	Al.		g Pl	he G	ly :	Pro	Glu	Ala 60	Ile	Arg	Arg	Ala
Ser 65	Val	Asn	Leu	Ala	Tr:		u H	is A	rg i	Arg	Phe 75	Pro	Trp	Thr	Phe	Asp 80
Val	Arg	Glu	Arg	Lec 85	As:	n Il	e I	le A	qa.	eys 90	Gly	Asp	Leu	Val	Phe 95	Ser

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly

Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His 115 $$120\$

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly 145 150 150 155

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His

Ser Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg \$245\$

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met 260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala 275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala 290 295 300

Lys Lys Asp 305

<210> 25

<211> 426

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(423)

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<210> 26

130

<211> 141

<212> PRT

<213> Neisseria meningitidis

<400> 26
Met Glu Gln Ser Gly Lys Phe Ser Trp Ser Ala Ala Ala Phe Trp Asp
1 10 15

Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr 20 25 30

Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys \$35\$

Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu 50 $\,$

Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser 65 70 75 80

Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys \$90\$

Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His 100 \$105\$

Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro 115 120 125

Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala 130 135 140

<210> 27

<211> 351

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(348)

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				ctg Leu 20							96
				aga Arg							144
				aat Asn							192
				tat Tyr							240
				ggt Gly							288
				cgt Arg 100							33
	ctg Leu	ege Arg	agg Arg 115	cac His	tga						35
<	210:	> :	28								
<	211:	> :	116								

<212> PRT

<213> Neisseria meningitidis

<400> 28 Met Gln Asn Gly Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu 1 15 15

Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp \$20\$

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  Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
  Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
  Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
  His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
 Leu Arg Arg His
          115
<210>
         29
<211>
        1404
<212> DNA
<213> Neisseria meningitidis
<220>
<221> CDS
<222>
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 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
                                     10
  tgo ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
  aga too tat tit too aga tat ato ota ooc git tog out tit aco tig
  Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
  cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca
  Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
  tgg cgg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac
  Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
                      70
  cag cgt gat gca gtg cgc gca cgg cam cam cam gcc mag gcc gcm ttc
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
                  85
  ctt ccc cat gta tee gec aat gec age tae cag ege cag eeg eea teg
  Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
             100
                                105
                                                   110
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att tot toc acc ogo gaa aca cag gga tgg ago gtg cag gtg gga caa

Ile S		Ser 115	Thr	Arg	Glu	Thr	Gln 120	Gly	Trp	Ser	Val	Gln 125	Val	Gly	Gln	
acc t	tta Leu 130	ttt Phe	gac Asp	gct Ala	Ala	aaa Lys 135	ttt Phe	gca Ala	caa Gln	tac Tyr	cgc Arg 140	caa Gln	agc Ser	agg Arg	ttc Phe	432
gat Asp 1	acg	cag Gln	gct Ala	gca Ala	gaa Glu 150	cag Gln	cgt Arg	ttc Phe	gat Asp	gcg Ala 155	gca Ala	cgc Arg	gaa Glu	gaa Glu	ttg Leu 160	480
ctg Leu	t t g Leu	aa a Lys	gtt Val	gcc Ala 165	gaa Glu	agt Ser	tat Tyr	ttc Phe	aac Asn 170	gtt Val	tta Leu	ctc Leu	agc Ser	cga Arg 175	gac Asp	528
acc Thr	gtt Val	gcc Ala	gcc Ala 180	cat His	gcg Ala	gcg Ala	gaa Glu	aaa Lys 185	gag Glu	gct Ala	tat Tyr	gcc Ala	cag Gln 190	cag Gln	gta Val	576
agg Arg	cag Gln	gcg Ala 195	cag Gln	gct Ala	tta Leu	ttc Phe	aat Asn 200	aaa Lys	ggt Gly	gct Ala	gcc Ala	acc Thr 205	gcg Ala	ctg Leu	gat Asp	624
att Ile	cac His 210	gaa Glu	gcc Ala	aaa Lys	gcc Ala	ggt Gly 215	tac Tyr	gac Asp	aat Asn	gcc Ala	ctg Leu 220	gcc Ala	caa Gln	gaa Glu	atc Ile	672
gcc Ala 225	gta Val	ttg Leu	gct Ala	gag Glu	aaa Lys 230	caa Gln	acc Thr	tat Tyr	gaa Glu	aac Asn 235	cag Gln	ttg Leu	aac Asn	gac Asp	tac Tyr 240	720
acc Thr	gac Asp	ctg	gat Asp	agc Ser 245	aaa Lys	caa Gln	atc	gag Glu	gcc Ala 250	Ile	gat	acc Thr	gcc Ala	aac Asn 255	ьец	768
t tg Leu	gca	cgc Arg	tat Tyr 260	Leu	ccc Pro	aag Lys	ctg Leu	gaa Glu 265	Arg	Tyr	agt Ser	ctg Leu	gat Asp 270	GIU	tgg Trp	816
cag Gln	Arg	275	Ala	tta Leu	tcc	aac Asn	aat Asn 280	His	gaa	tac Tyr	e egg	atg Met 285	Gir	cag Glr	ctt Leu	864
gcc Ala	Lev 290	ı Glı	ago 1 Ses	ago r Ser	Gly	Glr 295	Ala	ctt Lev	cgg Arg	g gca g Ala	a gca a Ala 30	a Gin	aac Asr	ago Sei	cgc Arg	912
tat Tyr 305	Pro	ace Th	c gtt r Val	t tot l Ser	gcc Ala 310	His	gto Val	ggc Gl	tai	Caq Gli	n As	t aac n Asr	cto Let	tae 1 Ty:	t act Thr 320	960
t ca Ser	tc: Se:	r Al	g cas a Gl:	g aat n Asi 325	ı Ası	gad 1 Asj	tac Ty	cae r Hi	tai Ty:	r Ar	g gg g Gl	c aaa y Lys	gg Gl	g at y Me 33	g agc t Ser 5	1008
gto Val	gg L Gl	c gt y Va	a ca 1 Gl 34	n Le	g aa u As:	t tte	g cc	g ct	и Ту	t ac r Th	c gg r Gl	c gga y Gl	ga: Gl: 35	u Le	g tcg u Ser	1056
gg	aa	a at	c ca	t ga	a gc	c ga	a gc	g ca	a ta	c gg	g go	c gc	c ga	a gc	a cag	1104

									-	. ,								
	Gly	Lys	11e 355	His	Glu	Ala	Glu	Ala 360	Gln	Tyr	Gly	Ala	Ala 365	Glu	Ala	Glr	1	
	ctg Leu	acc Thr 370	gca Ala	acc Thr	gag Glu	cgg Arg	cac His 375	atc Ile	aaa Lys	ctc Leu	gcc Ala	gta Val 380	ege Arg	cag Gln	gct Ala	Typ		1152
										atc Ile							1	1200
										tcg Ser 410						Gl		1248
										ata Ile								1296
										gca Ala								1344
										999 91y								1392
			gaa Glu	taa														1404
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<2	12:	>]	PRT															
<2	13:	> I	Nei	sse	ria	me	nin	git	idi	s								
	Met	00> Th		su L	eu A	isn 1	Leu	Met	lle	Net	Gl:		р Ту	r G	ly :	Ele	Ser 15	Val
	Cy:s	: Le	u Ti		eu 1 20	hr :	Pro	Tyr	Leu	Gin 25		g1	u Le	u P	he s	Ser 30	Ala	Met
	Lys	s Se		yr P 35	he S	er :	Lys	Tyr	11e 40	Leu	Pro	o Va	l Se		eu 1 45	Phe	Thr	Leu
	Pro		n S 0	er L	eu s	er.	Pro	Ser 55	Vāl	Ser	Ala	a Ph		r L	eu :	Pro	Glu	Ala
	Trj 6		g A	la A	la (iln '	Gln 70	His	Ser	Ala	Ası		e G1	n A	a	Ser	His	Tyr 80

Thr	Leu 130	Phe	Asp	Ala	Ala	Lys 135	Phe	Ala	Gln	Tyr	Arg 140	Gln	Ser	Arg	Phe
Asp 145	Thr	Gln	Ala	Ala	Glu 150	Gln	Arg	Phe	Asp	Ala 155	Ala	Arg	Glu	Glu	Leu 160
Leu	Leu	Lys	Val	Ala 165	Glu	Ser	Tyr	Phe	Asn 170	Val	Leu	Leu	Ser	Arg 175	Asp
Thr	Val	Ala	Ala 180	His	Ala	Ala	Glu	Lys 185	Glu	Ala	Tyr	Ala	Gln 190	Gln	Val
Arg	Gln	Ala 195	Gln	Ala	Leu	Phe	Asn 200	avٍL	Gly	Ala	Ala	Thr 205	Ala	Leu	Asp
Ile	His 210	Glu	Ala	Lys	Ala	Gly 215	Tyr	Asp	Asn	Ala	Leu 220	Ala	Gln	Glu	Ile
Ala 225	Val	Leu	Ala	Glu	Lys 230	Gln	Thr	Tyr	Glu	Asn 235	Gln	Leu	Asn	Asp	Tyr 240
Tn	Asp	Leu	Asp	Ser 245	Lys	Gln	Ile	Glu	Ala 250	lle	Asp	Thr	Ala	Asn 255	Leu
Let	: Ala	Arg	777 260	Leu	Pro	Lys	Leu	31u 265	Arg	23.2	Ser	Leu	Asp 270	Glu	Trp
Gl:	Arg	11e 275	Ala	Leu	Ser	Asn	Asn 260	His	Glu	Tyr	Arg	Met 285	Gln	Gln	Leu
Ala	290		Ser	Ser	Gly	Gln 295	Ala	Leu	Arg	Ala	Ala 300	Cln	Asn	Ser	Arg
Ту: 3 С	Pro	Thr	Val	Ser	Ala 310	His	7al	Gly	Tyr	Gln 315	Asn	Asn	Leu	Tyr	Tnr 320
Se:	s Ser	Ala	Gln	Asn 325	Asn	Aep	Tyr	His	T}:r 330	Arg	Gly	Lys	Gly	Met 335	Ser
Va.	l Gly	Val	Gln 340		Asn	Leu	Pro	Leu 345		Thr	Gly	Gly	Glu 350	Leu	Ser
G1:	y Lys	355		Glu	Ala	Glu	Ala 360		Tyr	Gly	Ala	Ala 365		Ala	Gln
Le	370		Thr	Glu	Arg	H18		Lyz	Leu	Ala	Val 380		Gln	Ala	Tyr
Th 38	r Glu 5	Ser	Gly	Ala	Ala 390		Tyr	Gln	. Ile	Met 395		Gln	Glu	Arg	Val 400
Le	u Glu	Ser	Ser	Arg 405		Lys	Leu	Lys	Ser 413		Glu	Thr	Gly	Gln 415	
ту	r Gly	Ile	Arg		Arg	Leu	Glu	Val 425		Arc	Ala	. Arg	Gln 430		Val
Al	a Glr	Ala	Glu	Gln	Lys	Lev	Ala	Glr	. Ala	Arg	Tyr	Lys	Phe	Met	Leu

435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val 450 455 460

Phe Ala Glu 465

<210> 31 <211> 696

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(693)

<400> 31

atg aaa caa too goo oga ata aaa aat atg gat cag aca tta aaa aat 4 Met Lys Sin Ser Ala Arg Ile Lys Asn Met Asp Gin Thr Leu Lys Asn 1 10 15

aca tig ggc att ige geg off tha gec tit igh itt ggc geg gcc atc. 9 Thr Leu Gly lle Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile 20 25 30

goa toa ggt tat cac tig gas tat gas tac ggc tac ggt tat tot god \sim 144 Als Ser Gly Tyr Bis Lou Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Als \sim 35 \sim 46 \sim 48

gtg ggt got tig got tog git gia tit ita tia tig goa og: ggt l91 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Ala Arg Gly

the eeg ege got tot bea got got its etg att tae goe goe aca acc. 24: Phe Pro Arg Val Ser ser Val Val Len heu lie Tyr Val Gly Thr Thr

god ota tat tig dog gid ggi tig dig tat ggi gog dog tot tat dag 25% Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Sor Tyr Gln

ata gto ggt tog ata tig gaa ago aat oot goo gag gog ogt gaa titt 336. Tie Val Gly Ser Ile Leu Giu Ser Ass Pro Ala Glu Ala Arg Glu Phe 100 100 100 110

gto ggc aat cir coo ggg tog cir tat tit gtg cag gca tia tit tito. 384 Val Gly Asn Leu Pro Gly Ser Leu Tyr Pne Val Gln Ala Leu Phe Phe 115 115 116

att ttt ggd tig aca git igg aga tat igt gia tog ggg ggg gta itt 432 The Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe 130 140

got gac gta aaa aac tat aaa ogo ogs ago aaa ata tgg otg act ata 480 Ala Aap Val Lys Ash Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile 145 150 150 150 160

											gcc Ala 175	528
											att Ile	576
											cgc Arg	624
											gca Ala	672
ccg	tca	tgt	tgc	gcc	caa	gta	taa					696

<210> 32

225

<211> 231

<212> PRT

<213> Neisseria meningitidis

Pro Ser Cys Cys Ala Gln Val

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe 185 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr Pro Ser Cys Cys Ala Gln Val <210> 33 <211> 909 <212> DNA <213> Neisseria meningitidis <220> <221> CDS <222> (1)..(906) <400> 33 and ast get tac ggt the coa the one gat ace out the tog age ogg Met Asn Val Tyr Gly Pne Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg acc asa ggg ctg ttg sts sac ggt tac cat ttc acc gcc cac gcg acg Thr Lys Gly Leu Leu Ile Ash Gly Tyr His Phe Thr Ala His Ala Thr aut cut tog etg eeg sag act tug ggg oug oog gga gag eeg aac aat Asn Leu Ser Leu Pro Gli Tar Leu Sly Leu Pro Gly Glu Pro Asn Asn 192 aso att gto ago tig gog asg gag ggo tit ogg sog gog tig otg Asn The Val Ser Leu Ala Lys Gln Ala Bly Phe Arg Thr Ala Trp Leu tot aat caa gga atg tig ggg cat tit goo sac gaa att too acc tat 240 Ser Asn Gin Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr god ota ogo ago gat tat dog tgg tot acc daa agg ggt gat tat ggd Ala Leu Arg Ser Asp Tyr Pro Trp Pne Thr Gln Arg Gly Asp Tyr Gly asa age geg ggg tig age gas ege ett tig tig eeg geg tie aas egg 336 Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Beu Pro Ala Phe Lys Arg

gut tig ata gga aat gca ggo acg aag cot ogg cig att gig atg cac Val Leu lle Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His 115 125 ctg atg ggt tog cac agt gat tit ige aca ogt tig gat aag gat gog Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala

				cag Gln													480
				acc Thr													528
				gaa Glu 180													57€
				ggt Gly													624
				agc Ser													672
				gaa Glu													720
				Gly													768
				gat Asp 260													816
	aat Asn	aac Asn	ctt Let 275	gcc Ala	ttt Pre	ato	gac qaA	998 917 280	Ten esd	Ges Pra	gas	gac Asp	occ Pro 285	gcg Ala	Pro	tgg Trp	864
	tat Tyr	gcg Ala 290	G[]	aaa Lys	ggc Gly	aaa Lys	295 295	ast Thr	aaa Lys	ast Asn	acg	tet Ser 300	aaa Lys	aaa Lys	tga		909
<2	10:	> 3	34														
<2	11:	> 3	302														
<2	12:	> I	PRT														
< 2	213:	> 1	Veis	sser	ria	mer	ning	giti	.dis	3							
		00> 3 : Asi		Tyr	aly		Pro	Leu	Pro	. Asp 10		Pro	Phe	Leu	Ser 15	Arg	
	Thi	: Lys	Gly	/ Leu 20		Ile	Asn	gly	7;: 25		Phe	Thr	Ala	His 30	Ala	Thr	
	Ast	ı Let	ı Ser	Leu	Pro	sl:	Thr	Leu	Gly	Les	Pro	Gly	Glu	Pro	Asn	Asn	

Asn Leu Ser Leu Pro Gin Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn $\frac{40}{45}$ Asn Ile Val Ser Leu Ala Lys Gin Ala Gly Phe Arg Thr Ala Trp Leu $\frac{50}{55}$ Ser Asn Glu Ile Ser Thr Tyr

65					70					75					80
Ala	Leu	Arg	Ser	Asp 85	Tyr	Pro	Trp	Phe	Thr 90	Gln	Arg	Gly	Asp	Tyr 95	Gly
Lys	ser	Ala	Gly 100	Leu	Ser	Asp	Arg	Leu 105	Leu	Leu	Pro	Ala	Phe 110	ГЛS	Arg
Val	Leu	Ile 115	Gly	Asn	Ala	Gly	Thr 120	Lys	Pro	Arg	Leu	11e 125	Val	Met	His
Leu	Met 130	Gly	Ser	His	Ser	Asp 135	Phe	Сув	Thr	Arg	Leu 140	Asp	Lys	Asp	Ala
Arg 145	Arg	Phe	Gln	Tyr	Gln 150	Thr	Glu	Lys	Ile	Ser 155	Cys	Tyr	Val	ser	Thr 160
Ile	Ala	Gln	Thr	Asp 165	Lys	Phe	Leu	Glu	Asp 170	Thr	Val	Lys	Ile	Ьеи 175	Asn
Glu	Asn	Lys	Glu 180	Ser	Trp	Ser	Leu	Val 185		Phe	Ser	Asp	His 190	Gly	Leu
Met	His	Val 195	Gly	Lys	Gly	Gly	Glu 200	Arg	Thr	Leu	Thr	His 205	Gly	Ala	Trp
Lys	Arg 210		Ser	Tyr	Gly	Val		Leu	Val	Lys	Ile 220	Ser	Ser	Asp	Asp
Thr	Arg	Arg	Glu	Met	Ile 230	Lys	Val	Arg	Arg	Ser 235	Ala	Phe	Asr.	Phe	Leu 240
Arg	Gly	Phe	Gly	Ser 245		Tar	Gl;	ile	Glu 250	Thr	Asp	Glu	. Leu	Pro 253	Yab
Asp	Gly	Tyz	Asp 260		Trp	Gly	As:	. Val	Fro	Asp	val	. Glr	270	Glu	Gly
Asr	Ast	1 Leu 275		Phe	: Ile	Asp	Gly 280	Let	Pro) As	gaA c	285	als	Pro	Tr
Zyr	290		/ Lys	: Gly	, Lys	5 Ser 295	Thr	- Lys	: Ası	ı Thi	300	c Lys	. Lys	i	
210	>	35													
211	>	864													
212	>	DNA													
213	> :	Nei	sse:	ria	mer	ing	itio	dis							
220	>														

CDS

(1)..(861)

<221>

<222>

<400> 35 atg atg agt caa cac tot got gga goa ogt tto ogt caa got gtg aaa Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys gaa tog aat cog ett gee gte gee ggt tge gte aat get tat ttt gea Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala ega ttg gee acc caa age ggt tte aaa gee ate tat etg tee gge gge Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly ggc gtg gca gcc tgt tct tgc ggt acc cct gat ttg ggc att acc aca Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr atg gas gat gtg etg ate gac gea ega ege att aeg gac aac gtg gat Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn att god ogt acc att ogd aad tot gaa ogd god got got goa gog gto 336 Ile Ala Arg Thr Ile Arg Asn Pne Glu Arg Ala Gly Val Ala Ala Val cac atc gaa gat cag gta gog caa aaa cgc tgc ggc cac cgt cog aac His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn ass goo att gts tot ass gat gas stg gto gad ogt atc ass got goo Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala già gat gog ego git gat gag aac tie gig att atg gog egi acc gat Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp gog oig gog gia gaa ggt tig gat god got atd gaa ogd god daa got Ala Deu Ala Val Glu Gly Deu Asp Ala Ala Ile Glu Arg Ala Gin Ala tgt gto gaa goo ggt goo gac atg att tto cot gaa goo atg aco gat Cys Vai Glu Ala Gly Ala Asp Met Ils Phe Pro Glu Ala Met Thr Asp Tig aac aig tac ogc caa tit goa gai gog gig aaa gig coo gig lig Leu Ash Met Tyr Arg Cln She Ala Asp Ala Val Lys Val Fro Val Leu . 02 gog aac att acc gag tot ggt too act oog ett tat acc caa age gag Ala Asm Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Glm Ser Glu ctg got gam ame gge gtg teg etg etg etg tat eeg etg tem teg tte Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe cgt gca gca ago aaa gco gct ctg sat gtt tac gaa gcg att atg cgc

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg

gat ggc act toa ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga Asp Gly Thr Ser Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg got gta oga gca tot gaa ota toa tgo ott oga gca aaa act gga taa Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly <210> 36 <211> 287 <212> PRT <213> Neisseria meningitidis <400> 36 Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp Thr Pro Leu Leu Val Asp Ile Asp Val Sly Trp Gly Gly Ala Phe Asn 85 90 95 Die Ala Arg Tor Die Arg Ast Phe Glu Arg Ala Gly Val Ala Ala Val His Tie Glu Asp Gin Val Ala Gin Lys Arg Cys Gly His Arg Pro Ass Lys Ala Tie Val Ser Lys Asp Glu Met Val Asp Arg Tie Lys Ala Ala Val Asp Ala Arg Val Asp Glu Ash Phe Val Tie Met Ala Arg Thr Asp Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala Cys Val Glu Ala Gly Ala Asp Met Ile Pne Pro Glu Ala Met Thr Asp Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu Ala Asn Ile Thr Glu Phe Sly Ser Thr Pro Leu Tyr Thr Sln Ser Glu

Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg $245 \hspace{1cm} 250 \hspace{1cm} 255 \hspace{1cm}$

Asp Gly Thr Ser Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg 260 265 270

Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 37

<211> 921

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(918)

<400> 37

atg cct tog age aaa aac tgg ata aat tgt tto aaa aat gat tta cog 4. Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro 10 10 15

CIT to a gad tgc cit to a ada aat deg dat dgg tog tot gaa aad deg 5. Leu Ser App Cye Leu Ser Tor Asn Pro His Arg Ser Ser Glu Asn Pro

acc ccg acc ctc asa cct asa asa toc gtt gcg ctt tot gge gtt gcg 190 The Pro The Deu Lys Pro Dys Lyc Ser tal Ala Leu Ser Cly Val Ala 50

goo ggt aat acc got tie tgt acc git ggc ogt acc ggc aac gai tig 240 Ala Gly Acn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Ash Asp Leu

ago tat ogo ggt tad gad att otg gat thg god dad add tgt gag tht 288 Ser Tyr Arg Gly Tyr Asp Die Leu Arp Leu Ala Ghn Lys Cys Glu Phe

gaa gaa git goo cac eig eig ait cac ggo cat tia eec aac aaa ite — 336 Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe

gag ctg gcc gct tat aaa gcc aag ctt aaa toc atg cgc ggc ctg cct 384 Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro

atc cgt gtg att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg 432 Tie Arg Val Tie Lys Val Lee Glu Ser Leu Pro Ala His Thr His Pro

atg gac gtg atg ogt acc ggc gta icc atg ctg ggc tgt gtt cat oct 480 Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro 145 150

				agc Ser					528
				atc Ile					576
				gtt Val 200					624
				cac His					672
				ctg Leu					720
				cgc Arg					768
				gca Ala					816
				ctt Leu 280					864
				aca Thr				rva aec	912
Ser	tga								921

<210> 38

<211> 306

<212> PRT

<213> Neisseria meningitidis

<400> 38

Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro 1 10 15

Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro $20\,$ $\,25\,$

Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln $_{\mbox{35}}$

Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala 50 60

Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu 65 70 75 80

Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe 85 90 95

Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe 100 105 110

Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro

Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro 130 135 140

Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro 145 150 160

Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys \$165\$

Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser 180 185 190

His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly 195 200 205

Gly His Phe Let His Let Let His Gly Lys Arg Pro Ser Glu Ser His 210 $$\rm 215$ $$\rm 220$

Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe 225 \$230\$

Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp 245 250 255

Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys $260 \hspace{1cm} 265 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$

His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala 275 280 285

Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys 290 295 300

Lys Ser

<210> 39

<211> 945

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(942)

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				ata Ile												96
				ttc Phe												144
				tst Phe												192
att Ile 65	ttg Leu	ctt Leu	tgc Cys	cgt Arg	acc Thr 70	ggt	ttt Phe	acc Thr	aga Arg	cag Gln 75	att Ile	gcg Ala	gat Asp	att Ile	tca Ser 80	240
aga Arg	aag Lys	aaa Lys	gag Glu	gca Ala 85	att Ile	ttg Leu	ccg Pro	ttg Leu	ctg Leu 90	tta Leu	aaa Lys	gta Val	gca Ala	att Ile 95	tgt Cys	288
				att												336
caa Gln	tat Tyr	ggc Gly 115	aat Asn	gct Ala	gcg Ala	aat Asn	gta Val 120	gta Val	gtt Val	gta Val	tta Leu	atg Met 125	gca Ala	t cg Ser	gct Ala	384
gcc Ala	gta Val 130	tct Ser	gec Ala	ttg Leu	ata Ile	ttg Leu 135	gac Asp	agc Ser	ata Ile	ctg Leu	tta Leu 140	gat Asp	gaa Glu	cgt Arg	att Ile	432
tgc Cys 145	att Ile	tct Ser	tca Ser	gtc Val	gtc Val 150	ggt Gly	gtg Val	ggt Gly	ttg Leu	gca Ala 155	gta Val	ttg Leu	gjå äää	atc Ile	gca Ala 160	480
				act Thr 165												528
gca Ala	ctg Leu	gcg Ala	ggc Gly 180	tog Ser	ggc Gly	tac Tyr	ggt Gly	tgt Cys 185	ttt Phe	tcc Ser	gtt Val	ttg Leu	att Ile 190	aag Lys	aaa Lys	576
ttc Phe	ggc Gly	cta Leu 195	aac Asn	ggc Gly	ggt Gly	att Ile	tat Tyr 200	ttg Leu	aca Thr	cgg Arg	ata Ile	ttg Leu 205	atg Met	ttt Phe	ttt Phe	624
				ttg Leu											ata Ile	672
				tct Ser											ttg Leu 240	720

	att Ile							768
	gcg Ala							816
	ctg Leu 275							864
	Gly							912
	cga							945

<210> 40 <211> 314

305

<212> PRT

<213> Neisseria meningitidis

310

ú

Ala	Leu	Ala	Gly 180	Ser	Gly	Tyr	Gly	Cys 185	Phe	Ser	Val	Leu	11e		Lys	
Phe	Gly	Leu 195	Asn	Gly	Gly	Ile	туг 200	Leu	Thr	Arg	Ile	Leu 205		Phe	Phe	
Gly	Ser 210	Ile	Phe	Leu	Phe	11e 215		Ser	Leu	Glu	Gly 220		Glu	a Asp	Ile	
His 225	Trp	Gln	Trp	Ser	Phe 230	Ile	Pro	Pro	Leu	Leu 235		Leu	Ser	Leu	Leu 240	
Pro	Thr	Ile	Leu	Gly 245	Phe	Tyr	Cys	Thr	Thr 250	Lys	Ala	Leu	Asp	Tyr 255	Leu	
Ser	Ala	Ala	Lys 260		Gln	Val	Thr	Glu 265	Leu	Ala	Glu	Pro	Leu 270		Ala	
Ala	Val	Leu 275	Ala	Trp	Leu	Phe	Leu 280		Glu	Ile	Pro	Glu 285		Arg	Phe	
Phe	Val 290	Gly	Ala	Ile	Leu	11e 295	Ile	Ala	Gly	Гlе	Val 300		Ile	Asn	Gly	
Leu 305	Tyr	Arg	Pro	Leu	Leu 310	Lys	Arg	Ile	Glu							
210:	> 4	1														
211:	> 2	2610)													
212:		ONA														
								aia								
213:	> 1	METE	ssei	та	mer.	11119	ITLI	.uis								
220:	>															
221:	> (DS														
222			(2	607	')											
	0 > 4: act		820	C22	cat	t 20		aaa	cca	cto		~~-	200	an b		4.8
Met	Ala	Ala	Asn	Gln	Arg	Tyr	Arg	Lys	Pro	Leu	Pro	Gly	Thr	Asp	Leu	40
1				5					10					15		
gaa Glu	tac Tyr	tac Tyr	gac Asp 20	gcg Ala	cgt Arg	gcg Ala	gcg Ala	tgt Cys 25	gag Glu	gac Asp	atc Ile	aag Lys	ccc Pro	ggc Gly	tct Ser	96
Tyr	Asp	Lys 35	Leu	Pro	Tyr	Thr	ser 40	cgc Arg	Ile	Leu	gcg Ala	gag Glu 45	aat Asn	ttg Leu	gtc Val	14
aac Asn	cgc Arg 50	gcg Ala	gac Asp	aaa Lys	gtc Val	gat Asp 55	ttg Leu	ccg Pro	acg Thr	ctg Leu	caa Gln 60	agc Ser	tgg Trp	ctg Leu	ggt Gly	15
cag Gln 65	ctg Leu	att Ile	gag Glu	gga Gly	aaa Lys 70	cag Gln	gaa Glu	atc Ile	gac Asp	ttt Phe 75	cct Pro	tgg Trp	tat Tyr	ccg Pro	gcg Ala 80	24
caa	ara	ara	tac	cac		.++	cta	aaa	cac		~~~	tta	ata	ant.	++~	20

Ara	Va l	Val	Cve	His	aen.	Tle	Len	G1 v	Gln	Thr	a I A	Leu	Val	Asp	Leu	
5			-75	85	vab	110			90					95		
gca Ala	ggt Gly	ctg Leu	cgc Arg 100	gat Asp	gcg Ala	att Ile	gcc Ala	gaa Glu 105	aaa Lys	ggc Gly	ggc Gly	gat Asp	ect Pro 110	gcc Ala	aaa Lys	336
gtg Val	aat Asn	ccg Pro 115	gtg Val	gtt Val	gca Ala	aaa Lys	ccc Pro 120	agc Ser	ttc Phe	atc Ile	gtc Val	gac Asp 125	cac Hís	tct Ser	ctg Leu	384
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acg Thr	ccg Pro 210	His	gtc Val	gat Asp	gcg Ala	ctg Leu 215	ggc	gtg Val	att Ile	tcc Ser	gtg Val 220	Gly	gtg Val	ggc Gly	gga Gly	672
Leu 225	Glu	gcg Ala	gaa Glu	acc Thr	gtg Val 230	atg Met	ctg Leu	ggt Gly	cgc Arg	gcg Ala 235	Ser	atg Met	atg Met	cgc Arg	ctg Leu 240	720
Pro	gat Asp	att	gto Val	ggc Gly 245	Val	gag Glu	ctg	aac	ggc Gly 250	Lys	cgg	cag Gln	gcg Ala	ggc Gly 255	Ile	768
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gg 30	/ Ala	act Thr	gcc	gcg Ala	atg Met 310	Phe	gct Ala	att ille	gat Asp	gag Glu 315	ı Glı	a aco	att Ile	gat Asp	tat Tyr 320	960
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				ttg Leu												1104
				aac Asn												1152
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				gtc Val 405												1248
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aac Asn	tgc Cys	ttc Phe 435	999 Gly	ctg Leu	aaa Lys	ege Arg	aaa Lys 440	ecg	tgg Trp	gtc Val	aaa Lys	acc Thr 445	tcg Ser	ttt Phe	gcc Ala	1344
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ccc Pro 465	gaa Glu	atg Met	gaa Glu	aaa Lys	ctc Leu 470	ggc Gly	ttc Phe	ggt Gly	atc Ile	gts Val 475	gcc Ala	ttc Phe	gcc Ala	tgc Cys	acc Thr 480	1440
				atg Met 485												1488
atc Ile	atc	gac	ege Arg 500	Asp	ttg Leu	tac	gcc Ala	acc Thr 505	Ala	gta Val	tta Leu	tca Ser	ggc Gly 510	aac Asn	ege Arg	1536
			Gly	cgt Arg				Tyr					Phe			1584
		Pro		gtc Val								Ser			ttc Phe	1632
gat Asp 545	Ile	gaa Glu	aac Asn	gac Asp	gta Val 550	Leu	ggc Gly	gtt Val	gca Ala	gac Asp 555	Gly	Lys Lys	gaa Glu	ato	ege Arg 560	1680
ctç	aas	gac	att	tgg	cct	gco	gat	gaa	gaa	ato	gat	gco	gto	gtt	gcc	1728

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		ggc Gly 595														1824
		tcc Ser														1872
		gaa Glu														1920
		atc Ile														1968
		gcc Ala														2016
		aac Asn 675														2064
		acc Thr														2112
		ely age														2160
ggc Gly	gaa Glu	acc Thr	atg Met	ege Arg 725	atg Met	tgg Trp	gaa Glu	gcc Ala	atc Ile 730	gaa Glu	acc	tat Tyr	atg Met	aac Asn 735	ege Arg	2208
		Pro														2256
		gac Asp 755													gcg Ala	2304
att Ile	gtt Val 770	gcc Ala	gaa Glu	ggc	ttc Phe	gag Glu 775	cgt Arg	atc Ile	cac His	cgc	Thr 780	aac Asn	ctt Leu	atc	Gly	2352
	Gly										Thr				acc Thr 800	2400
ctg	caa	ctg	gac	ggt	acg	gaa	acc	tac	gac	gtg	gtc	ggc	gaa	cgo	aca	2448

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr 815

ccg cgc tgc gac ctg acc ctc gtg att cac cgt aaa aca gg gg gaa acc 2490

Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr 825

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Val Glu Val Pro Val Thr cys Arg Leu Asp Thr Ala Glu Glu Val Leu 835

gta tat gaa gcc ggc ggc gtg ttg caa cgg ttt gca cag gat ttt ttg
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 Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly 50

 Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65

 70

 Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu 85

 Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys 105

 Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp Pro Leu 125

 Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg 130

 Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp 145

 Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly

Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val

	Lys	Asn	Gly 195	Val	Ala	Phe	Pro	Asp 200	Thr	Cys	Val	Gly	Thr 205	Asp	Ser	His
	Thr	Pro 210	His	Val	Asp	Ala	Leu 215	Gly	Val	Ile	Ser	Val 220	Gly	Val	Gly	Gly
	Leu 225	Glu	Ala	Glu	Thr	Val 230	Met	Leu	Gly	Arg	Ala 235	Ser	Met	Met	Arg	Leu 240
	Pro	Asp	Ile	Val	Gly 245	Val	Glu	Leu	Asn	Gly 250	Lys	Arg	Gln	Ala	Gly 255	Ile
	Thr	Ala	Thr	Asp 260	Ile	Val	Leu	Ala	Leu 265	Thr	Glu	Phe	Leu	Arg 270	Lys	Glu
	Arg	Val	Val 275	Gly	Ala	Phe	Val	Glu 280	Phe	Phe	Gly	Glu	Gly 285	Ala	Arg	Ser
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	Tyr	Ala	Lys	Thr 340	Ala	Gly	Leu	Trp	Ala 345	qaA	Ala	Leu	Lys	Thr 350	Ala	Val
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	Ala	Gly 370		Ser	Asn	Pro	His 375	Ala	Arg	Phe	Ala	Thr 380	Ala	Asp	Leu	Ala
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	Pro	Asp	Gly	Ala	Val 405	Ile	Ile	Ala	Ala	Ile 410		ser	Cys	Thr	Asn 415	Thr
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	Pro	Gly 450		Lys	Val	Ala	Glu 455	Ile	Tyr	Leu	Lys	Glu 460		Gly	Leu	Leu
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	Ile	Ile	Asp	Arg	qaA	Leu	Tyr	Ala	Thr	Ala	. Val	Leu	Ser	GŢĀ	Asn	Arg

CTATAL CATAL

Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala

570

Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Al 515 520 525

500

Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe 530 540

Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg 545 555 550 560

Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala 565 570 575

Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe 580 580 590

Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg

Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu

Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro 625 630 635 640

Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala $645 \\ 650 \\ 655$

Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu 660 665 670

Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln 675 680 685

Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn 690 695 700

Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu 705 710 715 720

Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg 725 730 . 735

Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser 740 745 750

Ser Arg Asp Trp Ala Ala Lys Giy Val Arg Leu Ala Gly Val Glu Ala 755 760 765

Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly

Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr 785 790 795 800

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr 805 810 815

Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu 835 840 845 Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gin Asp Phe Leu

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gcg gga ago gca ego gac aaa ato cto ttg ego gta etc ggo ago eeg 14 Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro 45

gac coc tac ggc aag cag ata gac ggt ttg ggc aac gcc agt tog toc 193 Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Als Ser Ser Ser 50

acc ago asa gcc gtg att ttg gac asg tcc gas cgc acc gat cac gat Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp 65 70 80

gtc gat tac cft tic ggg caa gft toc atc gac aaa cct tit gtc gat Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp

tgg agt ggc aac tgc ggc aac etc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac ggc ccg 384 Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro 115 120 125

tgt acc gtc aaa atc tgg cag aaa acc atc ggc aaa acc att att gcc 432 Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 130 135 . 140

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14

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ctc Leu	gac Asp	ggc Gly	gta Val	acg Thr 165	ttc Phe	ccg Pro	gca Ala	gcc Ala	gaa Glu 170	gta Val	caa Gln	atc Ile	gaa Glu	ttt Phe 175	ctt Leu	528
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gaa Glu	aaa Lys	ttc Phe	gag Glu	aaa Lys 245	Ile	cgc Arg	gct Ala	tac Tyr	ggt Gly 250	gcg	ctg Leu	aaa Lys	atg Met	ggt Gly 255	Leu	768
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gco	tto A Phe	gto Val	. Ala	Pro	gcc Ala	gcc	gat Asp 280	Tyr	acc	gcc	tcc Ser	agt Ser 285	ggc	aaa Lys	acc	864
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aa: Ly: 30	s Let	g cad	cac His	gcg s Ala	g atg Met 310	Met	g ggt	aco Thi	gco Ala	tct Ser 315	: Val	gcc Ala	att Ile	gcg	acc Thr 320	960
gc Al	c gc	c gc	gte a Va	g cc 1 Pr 32	o Gly	ac;	g ctg r Lev	gto 1 Val	aac L Asi 330	ı Lei	goo l Ala	gca a Ala	G17	g gcg / Ala 33	g gga a Gly 5	1008
ac Th	g cg r Ar	t aa g Ly	a ga s Gl: 34	u Va	g cg	g Ph	e Gl	g car y Hi: 34.	s Pro	tc Se	c gg r Gl	e aca y Thi	Let 35	1 Ar	c gtc g Val	1056
99 G1	t gc y Al	a gc a Al 35	a Al	c ga a Gl	a tg u Cy:	t ca s Gl	g ga n As 36	b CJ.	a ca y Gl:	a tg n Tr	g ac p Th	g gcd r Ala 36	a Th	c aa r Ly	a gcg s Ala	1104
gt Va	t at 1 Me 37	t Se	c cg r Ar	c ag g Se	c gc r Al	a cg a Ar 37	g Va	g at 1 Me	g at t Me	g ga t Gl	a gg u Gl 38	y II	g gt p Va	c ag l Ar	g gtg g Val	1152
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<213> Neisseria meningitidis

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1	Ĺys	Gly	Val	Phe 20	Phe	Lys	Arg	Ser	Asp 25	Leu	Pro	Glu	Ala	A1a 30	Arg	Glu
1	Ala	Gly	Ser 35	Ala	Arg	Asp	Lys	Ile 40	Leu	Leu	Arg	Val	Leu 45	Gly	Ser	Pro
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	Val	Asp	Tyr	Leu	Phe 85	Gly	Gln	Val	Ser	Ile 90	Asp	Lys	Pro	Phe	Val 95	Asp
	Trp	Ser	Gly	Asn 100		Gly	Asn	Leu	Thr 105	Ala	Ala	Val	Gly	Ala 110	Phe	Ala
	lle	Glu	Glr 115		Leu	Val	Asp	Lys 120	Ser	Lys	Ile	Pro	Ser 125	Asp	Gly	Pro
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	His 145		l Pro) Met	Gln	Asn 150		Ala	Val	Leu	1 Glu 155	Thr	Gly	Asp	Phe	Glu 160
	Leu	Ası	o Gl	y Val	Thr 165		Pro	Ala	Ala	170	ı Val	Gln	Ile	Glu	Phe 175	Leu
	Asp	Pr	o Al	a Ası		Glu	Gly	/ Sez	: Met	Phe	e Pro	Thr	Gly	Asn 190	Leu	Val
	Asp	Gl	u Il 19		y Val	. Pro) Ası	n Ile 200		/ Arg	g Let	Lys	Ala 205	Thr	Leu	Ile
	Ası	1 Al 21		y Il	e Pro	Thi	. Val		e Let	ı Ası	n Ala	220	Asp	Leu	Gly	Tyr
	Th:		у Гу	s Gl	u Lei	230		p Ası	p Ile	a Ası	n Ası 23	n Asp	Ala	Ala	Ala	Leu 240
	Gli	ı Ly	s Ph	e Gl	u Ly:		e Ar	g Al	а Ту	r Gl	y Al	a Lev	ı Ly:	s Met	Gly 259	/ Leu

The Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val \$260\$

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  Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
                        310
  Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly
  Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
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 Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
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  Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
                                                                    240
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 Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
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Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
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9.0

85

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												agg Arg				432
												gct Val				480
												ecc				528
												ggt Gly				576
												cgc Arg 205				624
												ctg L e u				672
												cac His				729
												gcc			ggc	768
acg Thr	cac	cat His	ttt Pne 263	caa Gln	ggz Gly	ctg Leu	Pro	rrt Pne 265	Ala	ggc Gly	ggt Gly	ata Ile	acg Thr 270	cca Pro	ata Ile	816
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<213> Neisseria meningitidis

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Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile 50 55 50

Asp Leu Val Phe Ala Pro Gin Gly Gly Gly Phe Phe Gln Ala Asp Tyr $65 \hspace{1cm} 70 \hspace{1cm} 75 \hspace{1cm} 80 \hspace{1cm}$

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln 85 $90\,$ 95

Ile Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu 100 $$105\$

Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His 115 120 125

Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln 130 $$140\,$

Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala 145 150 160

Leu Gln Arg Pro Arg Phe Pro Pne Gln Ile Gln Thr Pro Phe Phe Thr 165 170 175

Glu Ser Gly Ile Phe Arg Arg Arg Ash Lyb Val Ash Gly Ile Gly Lys 180 185 190

Arg Tyr Arg Gly Asn Ala Asp The Gly Gln Fhe Leu Arg Thr Phe Ala 195 \$200\$

Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala 210 215 220

Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His 225 230 235 240

Ile Lys Ser Ala Arg Ris Ala His Ile Ala Val His Ala Leu His Gly 245 250 255

Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile 260 265 270

Arg Ile Asp Arg Phe Ala Val Gin Phe Arg Leu Ile His Gly Thr Gly 275 280 285

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cat His	cag Glr	gge Gly	aaa Lys	ctg Leu 85	gtg Val	gaa Glu	att	pro	gtc Val 90	tgc Cys	tac Tyr	Gly ggc	ggc	gaa Glu 95	tac Tyr	288
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											acc					384
		Gln									ttg Leu 140					432
cac His 145	Thr	Pro	ege Arg	cgt Arg	gcc Ala 150	gtg Val	pro	aga Arg	acg	ser 185	gtt Val	Pro	gos	ggt Gly	Ser 160	480
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   Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
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Gly Thr Ala Ala 11e Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
   gaa ogg gat acg ocg tit igt oto acc ggt god gig tal dag gog gaa
Glu Arg Asp Thr Pro Phe Cys Lei Thr Gly Ala Val Tyr Gln Ala Glu
   tig gao ggo gas cog gto tat tog tat tig ogt tat acc goo ogo aas Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Trr Ala Arg Lys
    ggg cag acc tig ass and gtg cgt gcc gtg cag ggc atg tac ggc tat
    Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
    gtg tgc gtg gcg ggc gga ttt gat gtg ccg gaa gtg atg ggt tcg aga
    Val Cys Val Ala Gly Gly Pne Asp Val Pro Glu Val Met Gly Ser Arg
    ago aco gao ctg aaa goo ggt tto ggo ggo cat cag ggo aga atg ctg
Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
    caa aaa ggo gat tat oto ooc ato ggo aaa ggt geg cag gaa ttg too
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Gin Lys Gly Asp Tyr Leu Pro Ile Giy Lys Gly Ala Gln Glu Leu Ser

asa gio ggo att goc ocq ata ocg itt acc gat acc atc cac cit git Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val 165 ct Cog gas tat goc gct tit act gos as as ggo cgt ocg aat cig Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu

185

190

150

7.80

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Ser His Kla Val Gln Kla Gly Thr Val Gln Val Pro Pro Gly Gly Lys 225 225 226 227 228 229 229 229 220 22		ege Arg	Phe	gac Asp	gga Gly	cag Gln	ccg Pro	Leu	acc Thr	ctg Leu	teg Ser	caa Gln	Pro	ttg Leu	gaa Glu	atg Met	ctg Leu	672
Pro Tile Tile Leu Leu Ala Asp Ala Gin Thr Thr Gly Gly Tyr Pro Dys 245 atc gct acc gtt gcc gcc gcc gat ttg ggc agg ctg gca cag gtg cgc lie Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gin Val Arg 265 ttc ggc agc aaa gtc aas ttc aaa ata atc ggc ttg asa gaa gcc acc Phe Gly Ser Lys Val Lys Phe Lys Tile Cle Gly Leu Lys Glu Ala Thr 265 gcc ctg cgg cgc aaa ac caa gtc tat ctg sac cas ats cgg aga atc 261 alac Arg Arg Lys Asn Can Val Tyr Leu Asn Gin Tile Arg Arg Tile 290 acc cat gas gcs ggt tgs 291 acc cat gas gcs ggt tgs 292 acc cat gas gcs ggt tgs 300 acc cat gas acc acc acc acc acc acc acc acc acc a		Ser	cac His	gct Ala	gtt Val	cag Gln	Ala	gga Gly	acc Thr	gtg Val	cag Gln	Val	pro	ccc Pro	ggc Gly	ggc Gly	Lys	720
The Ala Thr Val Ala Ala Ala Ala Asp Leu olly Arg Leu Ala Gln Val Arg 260 ttc ggc agc aaa gtc aaa ttc aaa ata atc ggc ttg asa gaa gcc acc Phe Gly Ser Lys Val Lys Phe Lys The lie Gly Leu Lys Glu Ala Thr 275 gcc ctg cgg cgc aaa aac caa gtc tat ctg sac cas ata cgg aga atc Ala Leu Arg Arg Lys Asn Can Val Tyr Leu Asn Gln The Arg Arg The 290 acc cat gaa gca ggt tga 300 acc cat gaa gca ggt tga 705 Thr Has Glu Ala Gly 300 2210 > 50 2211 > 309 2212 > PRT 2213 > Neisseria meningitidis <400 > 50 Met The His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asg Thr 1 1 5 15 Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met 25 Asp Thr Val Ala Leu Ala Ala Gly 4 sn Ile Leu Leu Cly Asn Asp Glu 45 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe 50 Glu Arg Asp Thr Pro Phe Cye Leu Thr Gly Ala Val Tyr Gln Ala Glu 65 Glu Arg Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys 95 Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr		ccg Pro	att Ile	atc Ile	ctg Leu	Leu	gcc Ala	gat Asp	gcg Ala	caa Gln	Thr	acc Thr	ggc Gly	ggt Gly	tat Tyr	Pro	aaa Lys	768
Phe Gly Ser Lye Val Lye Phe lys The lie Gly Leu Lye Glu Ala Thr 275 gct cty Cgg cgc aaa aac caa gtc tat cty sac caa ata cgg aga atc Ala Leu Arg Arg Lye Asn can Val Tyr Leu Asn Gln Ile Arg Arg Ile 290 acc cat gaa gca ggt tye 300 acc cat gaa gca ggt tye 305 2210		atc Ile	gct Ala	acc	Val	gcc Ala	gec Ala	gcc Ala	gat Asp	Leu	ggc Gly	agg Arg	ctg Leu	gca Ala	Gln	gtg Val	cgc Arg	816
Ala Leu Arg Arg Lys Asn d.n Val Tyr Leu Asn Gin Ile Arg Arg Ile 290 acc cat gas gca ggt tgs The Mis Glu Ala Gly 305 2210> 50 2211> 309 2212> PRT 2213> Neisseria meningitidis <400> 50 Met Ile His Val Ser Ala Val Glr Ala Pro Ala His Ile Gln Asp Thr 1		ttc Phe	ggc	Ser	aaa Lys	gtc Val	aaa Lys	ttc Phe	Lys	ata Ile	atc	ggc Gly	ttg Leu	Lys	gaa Glu	gcc Ala	acc Thr	864
The Has Glu Ala Gly 2210> 50 2211> 309 2212> PRT 2213> Neisseria meningitidis 2400> 50 Met Ile His Val Ser Ala Val Glr Ala Fro Ala His Ile Gln Asp Thr 1 16 Gly Arg Tyr Gly His Arg Alg Tyr Gly Ile Gly His Ala Gly Ala Met 20 Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu 40 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe 50 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu 65 Clu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys 50 Gly Gln Thr Leu Lys Met Val Arg Rla Val Gln Gly Met Tyr Gly Tyr		gcs Ala	Leu	cgg Arg	cgc Arg	aaa Lys	aac Asn	G_n	gtc Val	tat Tyr	ctg Leu	aac Asn	Gin	ata Ile	cgg Arg	aga Arg	atc Ile	912
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Met Ile His Vel Ser Ala Val Gir Ala Pro Ala His Ile Gin Asp Thr 1																		
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65 70 75 80 Leu Asp Gly Glu Pro Vai Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys 95 95 Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr		Gly	Thr 50	Ala	Ala	lle	Glu		Ala	Leu	Gly	Gly		Met	Leu	Val	Phe	
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 Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
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 Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu
  Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys
  Pro Ile Ile Leu Leu Ala Asp Ala Glm Thr Thr Gly Gly Tyr Pro Lys
  The Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Glm Val Arg
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  Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
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25

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		Ser					Lei					Cly			agc Ser	672
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acc Thr	caa Gln 370	cag Gln	alt	tac Tyr	ctg Leu	cic Leu 375	atc Ile	tg: Cys	ttg Leu	att Tle	ser 380	got Ala	got Ala	gts Val	eet Pro	1152
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ccg ct Pro Le 53	u Leu														1632
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aat ac Asn Th															1728
gaa tt Glu Ph															1776
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agg to Arg Le															1968
gtg ga Val As	it got ip Ala	gca Ala 660	gca Ala	caa Cin	aag Lys	gtt Val	gto Val 665	tet Ser	ogt Arg	atg Met	ctg Leu	att Ile 670	cag Gin	aig Met	2016
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Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys 325 330 335 Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser 340 350

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- Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro $_{\rm 370}$ $_{\rm 375}$
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- Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 415
- Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn
- Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
- Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn $450 \,$ 455 $\,$ 460
- Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 465 470 475
- Gly lie Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala $485 \ \ \, 490 \ \ \, 495$
- Arg Val Leu Ser Ala The Pro Glu Met Gln Ser Met Ile Val Ala Glu $500\,$
- The Ash Pro Ala Tyr arg Ser Leu The Ala Asp Giu Pro Ghn The Ala 515 \$525
- Pro Leu Leu Gin Asp Lys Arg Val Giu Ile Val Leu Asp Asp Gly Arg 530 535
- bys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met 545 \$550\$
- Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala 565 575
- Glu Phe Leu Lys Gln Val Gln Ser Ris leu Thr Pro Asp Gly Tle Val 580 585
- Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His 595 600 605
- Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala 610 $\,$ 620 $\,$
- Thr Pro Val Val Phe Pro Ash Lys Glu Leu Leu Lys Gln Arg Leu Ser 625 630 635 640
- Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
- Val Asp Ala Ala Ala Glm Lys Val Val Ser Arg Met Leu Ile Glm Met 650 665 670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile 675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile 690 695

<210> 53

<211> 1040

<212> PRT

<213> Neisseria meningitidis

<400> 53

Cys Leu Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly
1 5 10 15

Gly Thr Gly Iie Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala 20 25 30

Ala Val Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser $35 \hspace{1cm} 40 \hspace{1cm} 45$

Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala 50 $$\rm 55$ 60

Lys Ile Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn 65 70 75 80

Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu 85 90 95

Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly 100 \$105\$

Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu

His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys 130 \$135\$

Glu Ala Pro Glu Asp Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp 145 \$150\$

Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His 165 170 175

Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly

Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr

Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser 210 215 220

Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg 225 \$230\$

- Ile Val Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp 245 250 255
- His Phe Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu $260 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$
- Ala Tyr Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln 275 280 285
- Gln Ser Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met 290 295 300
- Leu Phe Ile Phe Ser Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr 305 \$310\$
- Leu Thr Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile 325 330 335
- Thr Val Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn 340 345 350
- His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala 355 360 365
- Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Iie Aia Gly Thr Ser
- Phe Ser Ala Pro IIe Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys 385 \$390
- Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr 405 410 415
- Ala Gin Asp Ile Gly Ala Val Giy Val Asp Ser Lys Phe Gly Trp Gly 420 \$425\$
- Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe 435 440 445
- Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser 450 460
- Phe Arg Ash Asp Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly 465 470 475 480
- Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile \$485\$
- Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met 500 505 510
- Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly 515 520 525
- Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg 530 540
 - Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly

 545
 550
 555
 560

- Gly Glu Gly Thr Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp \$555\$
- Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys 580 585 590
- Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser
- Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr
- Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly 625 630 635
- Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala 645 650 655
- Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His $_{660}$
- Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu
- Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala 690 700
- Ala Asp Arg Thr Asp Met Pro Giy Ile Arg Pro Tyr Gly Ala Thr Phe 705 710 720
- Arg Ala Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg 725 730 735
- Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala 740 740
- His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu $755 \\ 760 \\ 765$
- Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp $770 \hspace{1cm} 775 \hspace{1cm} 780 \hspace{1cm}$
- Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser 785 $$ 790 $$ 795 $$ 300
- Thr Glr Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala 805 810 815
- Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala 820 825 830
- Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp 835 840 845
- Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr 850 \$850
- Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly 865 870 875

Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn 885 . . 890 895

Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg 900 905 910

Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu 915 920 925

Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala $930 \\ 935 \\ 940$

Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala 945 950 955

Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr 965 970 975

Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg $980 \hspace{1.5cm} 985 \hspace{1.5cm} 990$

Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu 995 1000 1005

Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser 1010 1015 1020

Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe 1025 \$1030\$ 1035 \$1040

<210> 54

<211> 858

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(855)

<400> 54

atg tot gaa gaa aaa ttg aaa atg agt tto gag oca aco gta ato gaa 48 Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu 1 1 15

cat tig ggt gta aag atg tat tig cac act gtt cct gcg att gcc gag 96 His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu 20 25 30

ttg ata gcg aat gcc tac gat gca tgt gct acg gaa gtg gaa gtt agg 144 Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg 35 40 45

tta ttc gat aaa cog gag cat aaa atc gtt att aaa gat aat ggc ata 192 Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile 50 55 55

	atg Met															240
	aga Arg															288
	aaa Lys															336
	gaa Glu															384
	tat Tyr 130															432
	aaa Lys															480
	acc Thr															528
	cat His															576
	gta Val															624
	tat Tyr 210															672
gca Ala 225	acc Thr	aat Asn	att Ile	tca Ser	teg Ser 230	tta Leu	tct Ser	tca Ser	aaa Lys	ttc Phe 235	gaa Glu	cag Gln	tat Tyr	gaa Glu	tac Tyr 240	720
agc Ser	gga Gly	tta Leu	ata Ile	caa Gln 245	ggt Gly	aag Lys	ttc Phe	att Ile	aca Thr 250	acg Thr	gaa Glu	aaa Lys	cct Pro	tta Leu 255	aag Lys	768
	aat Asn															816
atg Met	ccc Pro	gag Glu 275	ttt Phe	ttc Phe	act Thr	gat Asp	agc Ser 280	gaa Glu	tcc Ser	agc Ser	cat His	Phe 285	taa			858

<210> 55

<211> 285

<212> PRT

<213> Neisseria gonorrhoeae

<400> 55
Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu
1 5 10 15

His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu $\frac{20}{20}$ $\frac{25}{30}$

Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg 35

Leu Phe Asp Lys Pro Glu His bys Ile Val Ile Lys Asp Asn Gly Ile 50 $\,$

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg 65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr 85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys 100 \$105\$

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu 115 120 125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe 130 135 140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr 145 150 150 155

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val \$165\$

Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile 180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu 195 200 205

Lys Tyr Asn Leu Val Thr Pro Gin Phe Glu Trp Glu Tyr Gln Asp Leu $_{\rm 210}$ $_{\rm 215}$

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr 225 230 235 240

Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys 245 \$250\$

Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn 260 265 270

Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe 275 280 285

<210> 56

<211> 1575

<212> DNA

<213> Neisseria gonorrhoeae

<220>
<221> CDS
<222> (1)..(1572

<2	22>	• (1).	. (1	572)											
	<400	> 56															
	atg Met 1	aaa Lys	aaa Lys	tcc Ser	Leu 5	ttc Phe	gtt Val	ctc Leu	ttt Phe	Leu 10	tat Tyr	tca Ser	Ser	Leu	Leu 15	Thr	48
	gcc Ala	agc Ser	gaa Glu	atc 11e 20	gcc Ala	tat Tyr	ege Arg	tt Phe	gta Val 25	ttc Phe	gga Gly	att Ile	gaa Glu	acc Thr 30	tta Leu	ccg Pro	96
	gct Ala	gca Ala	aaa Lys 35	atg Met	gcg Ala	gaa Glu	acg Thr	ttt Phe 40	gcg Ala	ctg Leu	aca Thr	ttt Phe	atg Met 45	att Ile	gct Ala	gcg Ala	144
	ctg Leu	tat Tyr 50	ctg Leu	tt: Phe	gcg Ala	cgt Arg	tat Tyr 55	aag Lys	gct Ala	tcg Ser	cgg Arg	ctg Leu 60	ctg Leu	att Ile	gcg Ala	gtg Val	192
	ttt Phe 65	ttc Phe	gcg Ala	ttc Phe	agc Ser	atg Met 70	att Ile	gcc Ala	aac Asn	aat Asn	gtg Val 75	cat His	tac Tyr	gcg Ala	gtt Val	tat Tyr 80	240
	caa Gln	agc Ser	tgg Trp	atg Met	acg Thr 85	ggt	att Ile	aac Asn	tat Tyr	tgg Trp 90	ctg Leu	atg Met	ctg Leu	aaa Lys	gag Glu 95	gtt Val	288
	acc	gaa Glu	gtc Val	ggc Gly	Ser	gcg Ala	ggc Gly	gcg Ala	tcg Ser 105	Met	ttg Leu	gat Asp	aag Lys	ttg Leu 110	Trp	ctg Leu	336
	ect	gct Ala	ttg Lev 115	ı Trp	ggc Gly	gtg Val	gcg Ala	gaa Glu 120	Val	atg Met	ttg Leu	ttt Phe	tgc Cys 125	Ser	ctt Leu	gcc Ala	384
	aag Lys	tto Phe 130	Arg	e egt g Arg	aag Lys	acg	cat His	Phe	tct Ser	gcc	gat Asp	ata Ile 240	Leu	Phe	gcc Ala	ttc Phe	432
	Cta Let	ı Met	g cts	g ato u Met	g att	Phe 150	gtg Val	cgt	tcg Ser	tto Phe	gac Asp 155	Thi	aaa Lys	ca: Gl:	a gag n Glu	cac His 160	480
	gg Gl	att Y Ile	t to	g cco	aaa Lys 165	Pro	g aca	tac Tyr	ago Ser	c cgc r Arg	g Ile	aaa Ly:	a gco	aat As:	t tat n Tyr 17	ttc Phe	528
	ag Se	c tte	c gg	t tai y Ty: 18	r Phe	gte Val	1 Gl/ c ggg	g ege / Arg	g Val	l Le	g ccq u Pro	g ta c Ty:	t cas	tte 1 Le 19	u Ph	t gat e Asp	576
	tt Le	a ag u Se	c aa r Ly	g at	e Pr	t gt: o Va	g tto l Pho	aaa a Lys	a cas	g cc n Pr	t gc	t cc a Pr	a ag	c aa r Ly	a at	c ggg e Gly	624

		195					200					205				
caa Gln	ggc Gly 210	agt Ser	att Ile	caa Gln	aat Asn	atc Ile 215	gtc Val	ctg Leu	att Ile	atg Met	ggc Gly 220	gaa Glu	agc Ser	gaa Glu	agc Ser	672
												act Thr				720
tta Leu	acc Thr	cgg Arg	ctg Leu	tcg Ser 245	caa Gln	gcc Ala	gat Asp	ttt Phe	aag Lys 250	ccg Pro	att Ile	gtg Val	aaa Lys	caa Gln 255	agt Ser	768
												agt Ser				816
												ggc Gly 285				854
aat Asn	atg Met 290	ttc Phe	ege Arg	ctc Leu	gcc Ala	aaa Lys 295	gag Glu	cag Gln	ggc Gly	tat Tyr	gaa Glu 300	acg Thr	tat Tyr	ttt Phe	tac Tyr	912
												tta Leu				960
										Glr		ggc Gly				1008
												ttc Phe				1056
			Gln									caa Gln 365				1104
		Pro													ggc	1152
gaa Glu 385	. Ala	gat Asp	att	gtg Val	gat Asp 390	aag Lys	tac Tyr	gac Asp	Asn	Thr 395	Ile	cac	aaa Lys	acc Thr	gac Asp 400	1200
										Gln					ggc	1248
				Ala					His					Arg	caa Gln	1296
gat Asp	ato Ile	tac Tyr	aat Asn	caa Gln	ggc Gly	acg	gtg Val	Glr	ccc Pro	gac Asp	ago Ser	tat Tyr	att	gto Val	Pro	1344

435 440 445 ctg gtt ttg tac ago cog gat aag goo gtg caa cag got goo aac cag Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln got tit gog cot tgo gag att god tit cat cag cag ett toa acg tit Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe 465 1488 ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu 490 ggc tcg gta aca ggc aac ctg att acg ggc gat gca ggc agc ttg aac Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn att ogo aac ggo aag gog gaa tat gtt tat cog caa taa 7575 Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln 515 <210> 57 <211> 524 <212> PRT <213> Neisseria gonorrhoeae <400> 57 Met Lys Lys Ser Leu Phe Val Leu Phe Leu Tyr Ser Ser Leu Leu Thr Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Cly Ile Glu Thr Leu Pro Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val

Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr Gin Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe 135

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe

140

165 170 175

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp
180

Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly
195
200
205

Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser

210 215 220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 $$ 230 $$ 235 $$ 240

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser 245 250 255

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn $260 \hspace{1cm} 265 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$

Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275 280 285

Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290 295 300

Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys 305 \$310\$

Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn $_{\rm 325}$

Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350$

Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser \$355\$

His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370 380

Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp 385 390 395 403

Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly 405 410 425

Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln 420 \$425\$

Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro 435 440 445

Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln 450 455 460

Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe 465 470 475 480

Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn 500 505 510

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln 515 520

<210> 58

<211> 1314

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1311)

<400> 58

atg ctg acg ttt atc gga ttg ctg att atc ggg gtc atc gta tgg ctg 4 Met Leu Thr Phe 11e Gly Leu Leu I1e 11e Gly Val I1e Val Trp Leu 1 5 15

tig ctg acg gaa aaa gtg tog ccc atc atc gca tta atc tig gtg ccg 96 Leu Leu Thr Clu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro

ctg att ggg ggg ttg ctg ggg ggg ttt gat gta tcc caa tta aaa gaa la4 Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu

the tall tog ggo ggo acg ass tog gtg acg cag att gtg att atg for Phe Tyr Ser Gly Gly Tor Dys Ser Val Thr Gln Tie Val Ile Met Phe

and the too acc tig tit but ggs and and as gan gig ggs ong the 240 Met Phe Ser Ile Leu Phe Phe Cly Ile Met Ash Asp Val Gly Leu Phe 65 70 75 80

cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val

gea gtg agt gtg ggg acg ged tig gtg tig gtg gta gca dag tig gad 336 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala G.n Leu Aap

ggg gcg ggc gcg acg acg tit that tog gtc gtc ccc gcc cit tig ccg 384 Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro

ctt tac aag ogt otg cat atg aat oot tac etg etg ttt ttg etg etg 43: Leu Tyr Lys Arg Leu His Met Ash Pro Tyr Deu Leu Phe Leu Leu Leu 130 135 Leu

act too ago gog gog cta ato aac ctt ttg cog gog gog gog aco ato. 480 Thr Ser Ser Ala Gly Leu Tle Asn Leu Leu Pro Arg Gly Gly Pro Ile 145 150 155 160

999 Gly	cgg Arg	gtt Val	gca Ala	agc Ser 165	gtg Val	ttg Leu	ggc Gly	gca Ala	gat Asp 170	gtg Val	ggc Gly	gaa Glu	ttg Leu	tat Tyr 175	aaa Lys	528
cct Pro	ttg Leu	ttg Leu	acg Thr 180	gtg Val	caa Gln	att Ile	atc Ile	ggt Gly 185	gtg Val	gtg Val	ttt Phe	atc Ile	ctt Leu 190	gtg Val	ctg Leu	576
tcc Ser	ctg Leu	ttt Phe 195	ttg Leu	ggt Gly	gtg Val	cgt Arg	gaa Glu 200	aaa Lys	agg Arg	cgg Arg	att Ile	gtc Val 205	cgg Arg	gag Glu	ttg Leu	624
gly	gcg Ala 210	ttg Leu	Pro	gcc Ala	gtg Val	gog Ala 215	gat Asp	ttg Leu	ata Ile	aag Lys	ccg Pro 220	gcg Ala	ect Pro	ttg Leu	tcg Ser	672
gaa Glu 225	gaa Glu	gaa Glu	caa Gln	aaa Lys	ttg Leu 230	gcg Ala	Arg	ceg Pro	aaa Lys	ctg Leu 235	ttt Phe	tgg Trp	tgg Trp	aat Asn	gtc Val 240	720
ctg Leu	ctg Leu	ttt Phe	ttg Leu	gcg Ala 245	gcg Ala	atg Met	agc Ser	ctg Leu	ctt Leu 250	ttt Phe	tcg Ser	ggc Gly	atc Ile	ttc Phe 255	eeg Pro	768
ccg Pro	ggt Gly	tat Tyr	gta Val 260	ttt Phe	atg Met	ctg	gct Ala	gca Ala 253	acg Thr	gcg Ala	gcg Ala	ttg Leu	Ctt Leu 270	ttg Leu	aat Asn	816
tac Tyr	aga Arg	agc Ser 275	Pro	cag Gln	gaa Glu	cag Gln	atg Met 280	gag Glu	cgg	att	tat Tyr	gcc Ala 285	His	gcc	G1y ggs	864
ggo	gcg Ala 290	Val	atg Met	atg Met	gcg Ala	100 Ser 295	att Iie	stt Ile	ttg Leu	geg Ala	gca Ala 300		acg	ttt	trg beu	912
999 Gly 305	Tle	ttg Leu	aag Lys	ggc	geg Ala 310	Gly	atg Met	t t g Leu	gac Asp	gcg Ala 315	lie	ser Ser	aaa Lys	gac	Leu 320	960
gt <u>e</u> Val	cat His	atc Ile	ctg Lev	Pro 325	Asp	Ala	ttg Leu	Le.	Pro 330	Tyr	. Ter	cat His	Ile	gcc Ala 335	atc Ile	1008
ggt Gly	gtg Val	ltg Leu	99t Gly 340	/ Ile	. ccg	Leu	gag Glu	ttg Leu 349	. Val	ttg Le:	agt Sex	acg Thr	Gac Asy 350	Ala	tat Tyr	1056
tat Ty:	Phe	gga Gly 355	Let	tt: Phe	ecg Pro	att Ile	yal Yal	. Giv	ı caş	att 1 Ile	t acc	s tog ser 365	Gli	gcg Ala	g ggc a Gly	1104
Va:	370	Pro	Gl:	ı Ala	ı Ale	375	r Tyn	: Al:	a Mel	: Let	1 Il	0 0	/ Se:	: Ile	gre e Val	1152
gg! G1: 38:	Thi	tt: Phe	gt: Val	t acq	390 390	Let	teg 1 Se:	g dag	g gc	a Le	u Tr	g ato p Mei	E G1:	y Le	g ggt u Gly 400	1200

ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttc tgg 1248 Leu Ala Lys Leu Ser Met Gly Lys His 11e Arg Tyr Ser Phe Phe Trp 405 415

gcg tgg ggt ttg tcg ctg gcg ata ttg gtc agt tcg ata gcg gca gga 1296 Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly 420 420 430

atc gtg cct ctg ccg taa Ile Val Pro Leu Pro 1314

<210> 59

<211> 437

<212> PRT

<213> Neisseria gonorrhoeae

<400> 59

Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu 1 10 15

Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro 20 25 30

Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu 35 40 45

Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Die Val Die Met Phe

Met Pne Ser Ile Leu Phe Pne Gly Lle Met Ash Asp Val Gly Leu Phe 65 70 60

Arg Pro Met Tie Sly Gly Leu Tie Lys Leu Thr Arg Gly Asn Tie Val 85 90 95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp

Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro 115 120 125

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu 130 $$135\ \ \, 140\ \ \,]$

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile 145 156 156

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys 165 170 175

Pro Leu Deu Thr Val Glm Ile Ile Gly Val Val Phe Ile Leu Val Leu 180 185 190

Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu 195 200 205

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser 210 225

- Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Arn Val 225 230 240
- Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro $245 \hspace{1.5cm} 255 \hspace{1.5cm}$
- Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
- Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly $275 \\ 280 \\ 285$
- Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu 290 295 300
- Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu 305 \$310\$ 315 \$320
- Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
- Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr 340 345 350
- Tyr Phe Gly Leu Phe Pro Ile Val Glu Glu Ile Thr Ser Glu Ala Gly 355 $$360\$
- Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val 370 375 380
- Giy Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly 385 390 395
- Let Ala Lys Let Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp \$405\$
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- <212> DNA
- <213> Neisseria gonorrhoeae
- <220>
- <221> CDS
- <222> (1)..(1152)

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act tat ctq tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat

Thr	Tyr	Leu	Tyr 20	Gln	Lys	Pro,	Lys	Leu 25	Phe	Lys	Gly	Alą	Val 30	Arg	Asn	e - ,
	gaa Glu															144
gac Asp	cca Pro 50	acc Thr	gca Ala	ccg Pro	ctg Leu	ttt Phe 55	cat His	ctg Leu	cgt Arg	aaa Lys	aaa Lys 60	ggc Gly	gca Ala	atc Ile	gtt Val	192
ect Pro 65	aaa Lys	gaa Glu	gaa Glu	tac Tyr	gtc Val 70	gaa Glu	agt Ser	ttc Phe	gac Asp	gat Asp 75	t t g Leu	ggc Gly	aaa Lys	act Thr	cgc Arg 80	240
	cgt Arg															288
	tta Leu															336
	egt Arg															384
	ctt Leu 130															432
	gat Asp															480
	gcc Ala															528
	gat Asp													Leu		576
	ggt Gly												Arg			624
	Leu 210											Thr				672
	ggc					Glu					Lys				ata Ile 240	720
	agt Ser									Glu					Arg	768
ato	aac	gat	act	gee	gca	caa	att	get	gcc	atg	att	gco	gac		gto	816

	lle	Asn	Asp	Thr 260	Ala	Ala	Gln	Ile	Ala 265	Ala	Met	Ile	Ala	Asp 270	Pro	Val	88 L
	aat Asn	tat Tyr	gaa Glu 275	gcc Ala	ttc Phe	agt Ser	gaa Glu	gac Asp 280	ttt Phe	ctc Leu	ggc Gly	aaa Lys	gaa Glu 285	cgt Arg	acc Thr	gat Asp	864
	acc Thr	gct Ala 290	ttt Phe	cat His	ctc Leu	gaa Glu	cag Gln 295	ttc Phe	gcg	aat Asn	ecc Pro	aac Asn 300	get Ala	act Thr	ccg Pro	ctt Leu	912
	tca Ser 305	gac Asp	gac Asp	gtc Val	agg Arg	ttg Leu 310	aga Arg	tta Leu	aat Asn	gcc Ala	aat Asn 315	aat Asn	ttg Leu	gat Asp	acg Thr	ttg Leu 320	960
	gaa Glu	aag Lys	gga Gly	tat Tyr	ttg Leu 325	att	ggg Gly	aat Asn	gly ggg	atg Met 330	Lys	ata Ile	agc Ser	gta Val	gat Asp 335	gag Glu	1008
	ttg Leu	ggg Gly	aaa Lys	aaa Lys 340	Val	tta Leu	gaa Glu	cac His	atc Ile 345	ggt Gly	aag Lys	aat Asn	gaa Glu	ccg Pro 350	tta Leu	ttg Leu	1056
	ttg Leu	aaa Lys	aat Asn 355	Leu	ctg Leu	gtt Val	aac Asn	Phe 360	Asn	cag Gln	gca Ala	aaa Lys	His 365	Glu	gaa Glu	gtt Val	1104
	agg Arg	aag Lys 370	Leu	ato Ile	tat Tyr	cag Glm	ttg Leu 375	Tle	gag Glu	tta Let	gat Asp	Phe 380	Leu	gaa Glu	att	ttg Leu	1152
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<213> Neisseria gonorrhoeae

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile 100 105 110 Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr 130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu 145 \$150\$

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp 165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu 180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile 195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro 210 215

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile 225 \$230\$

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg 245 250 255

The Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val 260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp 275 280 283

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu 290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu 305 \$310\$

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu \$325\$

Let Gly Lys Lys Val Let Glu His Ile Gly Lys Asn Glu Pro Let Let 340 348 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val 355 360 365

Arg Lys Leu Ile Tyr Gin Leu Ile Glu Leu Rsp Phe Leu Glu Ile Leu 370 375 380

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ege e Arg G	aa a ln :	cc	agc Ser 20	ctg Leu	acg Thr	ggt Gly	aaa Lys	gtg Val 25	att Ile	ctg Leu	aca Thr	cga Arg	ccg Pro 30	ttg Leu	tca Ser	96
ttt t Phe S	ec :	cta Leu 35	tgg Trp	acg Thr	aca Thr	ttt Phe	gca Ala 40	tcg Ser	ata Ile	tct Ser	gcg Ala	tta Leu 45	ttg Leu	att Ile	atc Ile	144
ctg t Leu P	he 50	ttg Leu	ata Ile	ttt Pne	ggt Gly	aac Asn 55	tat Tyr	acg Thr	cga Arg	aag Lys	aca Thr 60	aca Thr	gtg Val	gag Glu	gga Gly	192
caa a Gln I 65	itt le	tta Leu	cct Pro	gca Ala	tcg Ser 70	GľÀ	gta Val	atc Ile	agg Arg	gtg Val 75	tat Tyr	gca Ala	ccg Pro	gat Asp	acg Thr 80	240
gly s	Car	att Ile	aca Thr	geg Ala 85	aaa Lys	ttc Phe	gig Val	gaa Glu	gat Asp 90	gga Gly	gaa Glu	aag Lys	gtt Val	aag Lys 95	gct Ala	288
Gly A	gac Asp	aag Lys	cta Leu 100	ttt Pne	geg Ala	ott Leu	tog Ser	acc Thr 135	tca Ser	egt Arg	ttc Phe	gge Gly	gca Ala 110	gga Gly	gat Asp	336
ago (gtg Val	cag Gln 115	cag Glr	cag Gln	t t g	aaa Lys	acg Trr 120	gag Glu	gca Ala	gtt Val	ttg	aag Lys 125	aaa Lys	acg Thr	ttg Leu	384
gca (gaa Glu 130	cag Glr	gaa Glu	ctg Leu	gjā āās	egt Arg 135	ctg Leu	aag Lys	ctg Leu	ata	His 140	Gly	aat Asn	gaa Glu	acg Tnr	432
cgc : Arg : 145	agc Ser	ctt Leu	aaa Lys	gca Ala	act Thr 150	gtc Val	gaa Clu	cgt Arg	tig	gaa Glu 155	. Ast	cag Gln	gaa Glu	cto Leu	cat His 160	480
att Ile	tcg Ser	caa Gin	cag Gln	ata Ile 165	gac Asp	ggt Gly	cag Gln	aaa Lys	agg Arg	Arg	att	aga Arg	ctt Leu	gcg Ala 175	gaa Glu	528
gaa Glu	atg Met	t t g Leu	cag Gln 180	Lys	tat Tyr	cgt Arg	ttc Phe	Cta Leu 185	Ser	gcc	aa: Asi	gat n Asp	gca Ala 190	ı Val	cca Pro	576
aaa Lys	caa Gln	gaa Glu 195	Met	atg Met	aat	gts Val	aag Lys 200	: Ala	gag Clu	ctt Let	tt: Le	a gaç u Glu 205	ı Glr	g aas	a gcc s Ala	624
aaa Lys	ctt Leu 210	Asp	gco Als	tac Tyr	cgc Arg	cga Arg 215	Gli	ı gaa	gto Val	gg:	g ct y Le 22	u Let	caç ı Glı	g ga: n Gl:	a atc u Ile	672
cgc a Arg T 225											o G]				ja	717

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<212> PRT

<213> Neisseria meningitidis

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Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser 20 25 30

Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile 35 40 45

Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr 65 70 75 80

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala 85 90 95

Gly Asp Lys Let Phe Ala Let Sor Thr Ser Arg Phe Gly Ala Gly Asp

Ser Val Gln Gln Gln Leu Lys Thr Glu A'a Val Leu Lys Lys Thr Leu 115 120 125

Ala Glu Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Clu Thr 130 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asr Gln Glu Leu His 145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu 165 170 175

Glu Mer Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala 195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile 210 215 220

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							ggg Gly									96
							ecc Pro 40									144
							gat Asp									192
							atc Ile									240
gca Ala	ata Ile	ccg Pro	aac Asn	gtc Val 85	gaa Glu	gtc Val	gga Gly	ogg Arg	cag Gin 90	gtt Val	gat Asp	Pro	toc Ser	25 27.8 9.5	ctg Leu	288
				Val			egt Arg									336
			Ser				ttt Phe 120									384
		Tyr					tat Tyr									432
agt Ser 145	Val	gta Val	tca Ser	gtg Val	gca Ala 150	aaa Lys	acg Thr	gca Ala	stg Leu	ggc Gly 155	aga Arg	cag Gln	gaa Glu	ttg Leu	tcg Ser 160	480
							gat Asp									528
tat	ctc	gtg Val	asa Lys 180	Ile	aaa Lys	ccc Pro	gac Asp	aaa Lys 185	Pro	acc Thr	ato	act	gca Ala 190	tac Tyr	ggt Gly	576
			Pro					Met					Asp		cta Leu	624
cac	gag Glu 210	aaa Lys	cgg Arg	cgg Arg	ctg Leu	tac Tyr 215	gaa Glu	tgg Trp	gta Val	ttg Leu	gag Glu 220	ccg Pro	att Ile	tac Tyr	agt Ser	672
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<213> Neisseria gonorrhoeae

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Met Ser Gly Arg Leu 225

<210> 66

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<212> DNA

<213> Neisseria gonorrhoeae

<220>

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							tt: Phe									192
							cac His									240
							att									288
							gtc Val									336
							ege Arg 120									384
Phe	att Ile 130	acc Thr	Leu	ccg	ttg Leu	Ltg Leu 135	ege Arg	gos Ala	Cac	gcc Ala	cgc Arg 140	tat Tyr	ttc Phe	Gly ggc	aaa Lys	432
Leu 145	gca Ala	ctg Leu	att Ile	cat His	Phe 150	gac	gcg Ala	cac H1s	acc	gac Asp 155	acc Thr	tac Tyr	gac Asp	aac Asn	Gly 160	480
							atg Met									528
							gta Val									576

	agt Ser	aaa Lys	aaa Lys 195	ttg Leu	cct Pro	ttt Phe	act Thr	gtg Val 200	ttg Leu	tcc Ser	gcc Ala	ccc Pro	aaa Lys 205	gtc Val	aat Asn	gaa Glu	624
				gaa Glu													672
				tac Tyr													720
	gcc Ala	ccc Pro	Gjà aaa	acc Thr	ggt Gly 245	acg Thr	ecc Pro	gta Val	tgc Cys	ggc Gly 250	ggc	ttg Leu	agc Ser	agc Ser	gac Asp 255	agg Arg	768
	gca Ala	tta Leu	aaa Lys	atc Ile 260	cta Leu	cgt Arg	ej aaa	ctg Leu	acg Thr 265	gat Asp	ctc Leu	gac Asp	atc Ile	gtc Val 270	ggt Gly	atg Met	816
	gat Asp	gtt Val	gta Val 275	gaa Glu	gtt Val	gcc Ala	scc Pro	tct Ser 280	tac Tyr	gac Asp	caa Gln	tcc Ser	gac Asp 285	att Ile	acc Thr	gct Ala	864
	ttg Leu	gcc Ala 290	ggc Gly	gcc Ala	aca Thr	att lie	gcc Ala 295	ttg Leu	gaa Glu	atg Met	ctt Leu	200 200	ctt Leu	caa Gln	ggt Gly	gcg Ala	912
		aag Lys		tga													924
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	Asn	i Asr	Phe	Gly 20		Leu	Arg	Leu	Pro 25		. Asn	Phe	: Met	Pro 30		Glu	
	Ser	His	: Ala		Trp	Val	. Ile	Thr 40		Val	Pro	Tyx	Asp 45		Ala	Val	
		50)		-		5.5		_			60			_	Ala	
	65	5				75)				75					Asp 80	
					8.5	5				90)				95		
	rne	: W13	ASI	100		, AS	Phe	· val	105		s Met	GIt	Ala	110		Gly	

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           115
                               120
   Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
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   Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
                                          155
   Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
   Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
   Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
                              200
           195
   Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
                          215
   Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
                       230
   Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Let Ser Ser Asp Arg
   Ala Leu Lys Ile Leu Arg Siy Leu Thr Asp Leu Asp Ile Val Gly Met
                                   268
  Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Sar Asp Ile Thr Ala
  Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Clm Gly Ala
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   Cys Leu Thr Leu Thr Pro Tyr Leu Glr. His Glu Leu Phe Ser Ala Met
                                                      30
   ada too tat tit too aaa tat ato ota ooo git toa cit tit aco tig 144
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Lys	Ser	Tyr 35	Phe	Ser	Lys	Tyr .	Ile 40	Leu	Pro	Val	Ser	Leu 45	Phe	Thr	Leu	
cca Pro	cta Leu 50	tcc Ser	ctt Leu	tcc Ser	cca Pro	ser 55	gtt Val	tcg Ser	gct Ala	ttt Phe	acg Thr 60	ctg Leu	cct Pro	gaa Glu	gca Ala	192
tgg Trp 65	cgg Arg	gcg Ala	gcg Ala	cag Gln	caa Gln 70	cat His	tcg Ser	gct Ala	gat Asp	ttt Phe 75	caa Gln	gcg Ala	tcc Ser	cat His	tac Tyr 80	240
cag Gln	cgt Arg	gat Asp	gca Ala	gtg Val 85	ege Arg	gca Ala	egg Arg	caa Gln	caa Gln 90	caa Gln	gcc Ala	aag Lys	gcc Ala	gca Ala 95	ttc Phe	288
ctt Leu	ccc Pro	cat Ris	gta Val 100	tcc Ser	gcc Ala	aat Asn	gcc Ala	agc Ser 105	tac Tyr	cag Gln	cgc Arg	cag Gln	ccg Pro 110	cca Pro	tcg Ser	336
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acc Thr	tta Leu 130	ttt Phe	gac qaA	gct Ala	gcc Ala	aaa Lys 135	ttt Phe	gca Ala	caa Gln	tac Tyr	ege Arg 140	caa Gln	agc Ser	agg Arg	ttc Phe	432
gat Asp 145	Thr	cag Gln	gct Ala	gca Ala	gaa Glu 150	cag Gln	egt Arg	tto Pne	gat Asp	gcg Ala 155	gca Ala	ege Arg	gaa Glu	gaa Glu	ttg Leu 160	480
ctg Leu	ttg	aaa Lys	got Val	gcc Ala 165	gaa Glu	agt Ser	tat Tyr	ttc Pne	aac Asn 170	gtt Val	tta Leu	ctc Leu	agc	cga Arg 175	gac Asp	528
Thr	gtt	gcc Ala	gcc Ala 180	cat His	gog	geg	gaa Glu	aaa 198	gag Glu	gct	tat Tyr	gcc Ala	Gln 190	cag Gl:	gta Val	576
agg Arg	Cag Glr	gcg Ala 195	Gln	got Ala	tta Leu	tto Phe	Ast Ast 200	Lys	ggt Gly	got Ala	gcc Ala	acc Thi 205	Ala	Leu	gat Asp	624
att Ile	210	Glu	gcc Ala	aaa Lys	gcc	ggt Gly 215	Tyz	gac : Asp	aat Asn	goo Ala	Leu 220	Ala	caa Glr	gas Glu	atc ile	672
Ala 225	· Val	ttg Lev	get Ala	gag Glu	aaa Lys 230	Glr	acc Thi	: nat	gaa 31u	aac As: 235	: Glr	ttg Lev	aac Asr	gad Asi	Tyr 240	720
Thi	gad Asi	tet Let	gat 1 Asi	Ser 245	Lys	caa Gl:	ato : Ile	gaç Gli	gcc : Ala 250	a Ile	a gat e Asi	Thi	gco Ala	25	ctg Leu	768
Le	ı Al	a Arg	260	r Lei	ı Pro	b Ly	Le:	263	ı Arş	g Ty:	r Se	r Lei	270	o Gir	tgg Trp	816
ca	g cg	at	ge:	e tta	a to	c aa:	aa:	c car	gaa	a ta	c cg	gate	g ca	g Ca	g ctt	864

Ghn Arg Ile Ala Leu Ser Ann Ann His Glu Tyr Arg Met Ghn Ghn Leu 275 286 geo ctg caa ago ago gga cag ggg ctt cgg gca gca cag aac ago cgc Ala Leu Ghn Ser Ser Gly Ghn Ala Leu Arg Ala Ala Ghn Ann Ser Arg 290 tat occ acc gtt tot gco cat gtc ggc tat cag aat aac ctc tac act 7yr Fro Thr Val Ser Ala His Val Gly Tyr Ghn Asn Ann Leu Tyr Thr 305 310 tca tot gcg cag aat aat gac tac cac tat cgg ggc aaa ggg atg agc 310 tca tot gcg cag aat aat gac tac cac tat cgg ggc aaa ggg atg agc 310 ser Ser Ala Ghn Ann Ann Ann Tyr His Tyr Arg Gly Lys Gly Met Ser 325 gtc ggc gta cag ttg aat ttg ccg ctt tat acc ggc gga gaa ttg tcg 315 gtc ggc gta cag ttg aat ttg ccg ctt tat acc ggc gga gaa ttg tcg 310 yal Gly Val Ghn Leu Ann Leu Pro Leu Tyr Thr Gly Gly Gly Lueu Ser 340 ggc aaa acc cat gaa gcc gaa gcg caa tac ggg gcc gca gaa gca cag 310 ggc aaa acc cat gaa gcc gaa gcg caa tac ggg gcc gca gaa gca cag 310 ggc aaa acc cat gaa gcc gaa cac aaa acc ggc gcc gca gaa gca cag 310 ggc aac gca acc gag cgg cac atc aaa ctc gcc gta cgc cag ga gcc ctg acc gca gcc gca gaa gcc ctg acc gca gcc gca gaa gcc ctg acc gca gcc gca gca gcc gca gca gcc gca gca	
Ala Leu Gin Ser Ser Gly Gin Ala Leu Arg Ala Ala Gin Asn Ser Arg 290 295 300 tat cee ace get tet gee cat gee gge tat cag aat aac etc tac act Tyr Pro Thr Val Ser Ala Ris Val Gly Tyr Gin Asn Asn Leu Tyr Thr 305 310 310 320 tea tet gee cag aat aat gac tac cac tat cgg gge aaa ggg atg age Ser Ser Ala Gin Asn Asn Asn Tyr Yarg Gly Lys Gly Met Ser 325 330 335 335 336 335 335 340 345 325 325 326 325 326 326 326 326 326 326 326 326 326 326	
Tyx Pro Thr Val Ser Ala His Val Gly Tyx Glh Asm Asm Leu Tyx Thr 310 toa tot gog cag aat aat gac tac cac tat cag ggc aaa ggg atg agc car Ser Ser Ala Gln Ann Asm Asm Tyr His Tyr Arg Gly Lys Gly Met Ser 330 gto ggc gta cag ttg aat ttg cog ott tat acc ggc gga gaa ttg tog Val Gly Val Gln Leu Asm Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 340 ggc aaa atc cat gaa gcc gaa gcg caa tac ggg gcc gcc gaa gca cag Gly Lys ILe His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln Ses 365 ctg acc gta acc gag cgg cac atc aca ggg gcc gcc gaa gca cag Gly Lys ILe His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln Ses 365 ctg acc gta acc gag cgg cac atc aca ctg gcc gta egc gct gta Leu Thr Ala Thr Glu Arg His lie Lys Leu Ala Val Arg Gln Ala Tyr 370 acc gaa agc ggt gcg gcs gct tac cac act atc agc gcc gca gac cgg gtt tac Leu Thr Ala Thr Glu Arg Hai Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 acc gaa agc ggt ttg aaa ttg act gac gca acc ggc cac gac cac gcc ttg gaa gta gca gca cac ggc atc gcg cac gaa cac ggc cac gac gcg ttg acc gca gac acc ggc cac gac cac gac cac gcg ttg acc gca gca cac gac cac gcg ttg acc gca gaa cac ggc cac gac cac gcg ttg acc gca gca cac gac cac gcg ttg acc gca gca cac gac cac gca cac gcg ttg acc gca gca cac gcg cac gac cac gca cac gcg ttg acc gca gca cac gcg cac gca cac g	2
Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 gto ggo gta dag ttg aat ttg dog oft tat add ggo gga gga ttg tog 101 yal Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 345 ggo aaa act dat gaa goo gaa ggo gaa tad ggg ggo ggo gao gao gaa gaa dag Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 ctg acc gaa acc gag ggo ga at aaa cta ggo gga ggo ggo ggo tat 11 Leu Thr Ala Thr Glu Arg His IL Lys Leu Ala Val Arg Gln Ala Tyr Thr Gly Ser Gly Ala Ala Ala Gln 375 acc gaa ago ggt ggo ggt tac daa atc atg ggo gaa gaa cgg gtt 12 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 195 ttg gaa ago ago dgt ttg aaa ttg aaa tog acc gaa acc ggo caa daa Leu Glu Ser Ser Arg Leu Lys Leu Ser Thr Glu Thr Gly Gln Gln 405 tac ggo atc ogo aac ogg ctg gaa gta ata cgg gcg gg ggo ggt tac ggo gta ggo ggt tac gaa acc ggo aac daa 12 tac ggo atc ogo aac ogg ctg gaa gta ata cgg gcg gg ggo ga gta 12 tac ggo atc ogo aac ogg ctg gaa gta ata cgg gcg gg cag gaa gta Tyr Gly Tle Arg Aen Arg Leu Glu Vil Ile Arg Ala Arg Gln Glu Val)
Val Gly Val Glin Leu Asm Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 340 340 350 350 350 350 350 350 350 350 350 360 360 360 365 365 365 365 365 365 365 365 365 365	8 (
Cly Lys ILe His Glu Âla Glu Âla Gln Tyr Gly Ala Ala Glu Ala Gln 355 ctg acc goa acc gag cgg cac acc asa cto goc gta cgc cag got tat Leu Thr Ala Thr Glu Arg His lle Lys Leu Ala Val Arg Gln Ala Tyr 370 acc goa agc ggt goc gcg cat cac aac atc atg goc caa goa cgg gtt Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 390 ttg goa agc agc cgt ttg asa ctg asa ctg acc goa acc ggo caa caa 12 Eeu Glu Ser Ser Arg Eeu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 405 tac ggc atc cgc acc gg ctg gaa gta ata cgg gcg cgg cag gac 12 Thr Glu Ser Ser Arg Eeu Lys Lys Ser Thr Glu Thr Gly Gln Gln 405 tac ggc atc cgc acc cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc 777 Gly Tle Arg Aen Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val	56
Leu Thr Ala Thr Glu Arg His lie Lys Leu Ala Val Arg Gln Ala Tyr 375 acc gas ago ggt ggg ggg cgt tac cas ato atg gog cas gas cgg gtt 12 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Tie Met Ala Gln Glu Arg Val 385 390 acc gas acc ggc cas cas 12 tg gas ago ago cgt ttg ass otg ass otg acc gas acc ggc cas cas 12 teu Glu Ser Ser Arg Leu Lys Leu Cys Ser Thr Glu Thr Gly Gln Gln 405 acc ggc ato cgc acc ggc gg gg gg gg agt ats cgg cgc gg cag gas gtc 12 Tyr Gly Tie Arg Aen Arg Leu Glu Vil Tie Arg Ala Arg Gln Glu Val	34
The Glu Ser Gly Als Als Arg tyr Gln Tle Met Als Gln Glu Arg Val 385 390 400 Tig gas ago ago agt tig ass org sas tog aco gas aco ggo cas cas Leu Glu Ser Ser Arg Leu Lys Des Lys Ser The Glu The Gly Gln Gln 405 415 Tac ggo ato ogo aso ogo org gas gts ats ogg ogo ogg cas gas gtc Tyr Gly Tle Arg Leu Arg Leu Gls Val Tle Arg Als Arg Gln Glu Val	52
Leu Glu Ser Ser Arg Leu Lys Ser Thr Glu Thr Gly Gin Gln 405 415 410 415 415 120 Ggc ato ogo aac ogo otg gaa gta ata ogo ogo ogo ogo gaa gta 212 Tyr Gly Ile Arg Ann Arg Leu Glu Val Ile Arg Ala Arg Gin Glu Val	00
Tyr Gly lle Arg Asn Arg Leu Glu Val lie Arg Ala Arg Gin Glu Val	45
470 475 430	96
gic cas gos gas cag ass org got cas gos ogg tat sas the stg otg 13 kla Gln kla Glu Gln Lys Leu kla Gln kla krg Tyr Lys Phe Mat Leu 45 445	44
got tat trg ege tig gig aas gag age gig tia gig tig gaa aeg gia 13 Ala Tyr Leu Arg Leu Val bys Gin Ser Gly Leu Gly Leu Glu Thr Val 450	92
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- Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala 50 55 60
- Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
- Gin Arg Asp Ala Val Arg Ala Arg Gin Gin Gin Ala Lys Ala Ala Phe
- Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
- Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125
- Thr Leu Phe Asp Ala Ala Lys Phe Ala Glr Tyr Arg Gln Ser Arg Phe 130 135 140
- Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu 145 $$150\,$
- Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp 165 170 175
- Thr Val Ala Ala His Ara Ala Slu Dys Glu Ala Tyr Ala Gln Gln Val 180 185 190
- Arg Gln Ala Gln Ala Leu Phe Asn lys Gly Ala Ala Thr Ala Leu Asp 195 200 205
- ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile 210 215 220
- Ala Val Leu Ala Clu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 \$230\$ 230 \$230\$
- Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 255
- Leu Ala Arg Tyr Leu Pro lys leu Glu Arg Tyr Ser Leu Asp Glu Trp \$260\$
- Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285
- Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 290 295 300
- Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 310 315
- Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 330 335

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   Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
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  Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
  goa toa ggt tat cac trg gaa tat gaa tac ggc tac ogt tat tot gcc
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  gtg ggc gct tig gct tog gtt gta ttt tta tta tta ttg gca cgc ggc
  Val Gly Ala Leu Ala Ser Val Val Pne Leu Leu Leu Leu Ala Arg Gly
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ata Ile	gt <i>c</i> Val	ggt Gly	tcg Ser 100	ata Ile	ttg Leu	gaa Glu	agc Ser	aat Asn 105	ect Pro	gcc Ala	gag Glu	gcg Ala	egt Arg 110	gaa Glu	ttt Phe	336
	gly															384
	Ttt Phe 130															432
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Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Ala Arg Gly $50 \\ 60$

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

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gcg Ala	The	ga: Asi	26	a Val	g ttg Lev	g gca	i Cti	g ac: 1 Th: 26!	c G11	g tt	c cto	g ego u Aro	Lys 27	5 G11	a cgc u Arg	816
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Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys 180 185

Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr

Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 210 215 220

Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 225 $$ 230 $$ 235 $$ 240

Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr

Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg $260 \hspace{1cm} 265 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$

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Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 290 295 300

Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu 305 \$310\$

Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr 325 330 335

Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr \$340\$

Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala \$355\$

Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly 370 375 380

Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro 385 390 395

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- Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile 485 490 495
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- Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 610 620
- Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp 625 630 635 640
- Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp 660 665 670
- Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg 675 680 685
- Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu $690 \hspace{1cm} 695 \hspace{1cm} 700 \hspace{1cm}$
- Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly 705 710715720
- Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys 725 730 735
- Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser $740 \ \ \, 745 \ \ \, 750$
- Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile 755 760 765
- Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met
- Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu 785 790 795 800

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Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
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Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val

Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val 835 \$840\$

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gog gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144 Ala Gly Ser Ala Arg Asp Lys 11e Leu Leu Arg Val Leu Gly Ser Pro 35 40 45

gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc 192 Asp Pro Tyr Gly Lys Gln fle Asp Gly Leu Gly Asn Ala Ser Ser Ser 50 55 60

acc agc aag gog gtg att ttg gac aag tcc gaa cgc gcc gat cac gat Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp 65 70 88

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa ect ttt gtc gat Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 90

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336 Trp Ser Gly Aen Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala

atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac ggc atc 184 Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile 125

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cat His 145	gta Val	ccg Pro	atg Met	caa Gln	aac Asn 150	ggc Gly	gca Ala	gtt Val	ttg Leu	gaa Glu 155	aca Thr	ggc Gly	gat Asp	ttt Phe	gag Glu 160	480
ctc Leu	gac Asp	ggc Gly	gta Val	acg Thr 165	ttc Phe	ceg Pro	gca Ala	gcc Ala	gaa Glu 170	gta Val	caa Gln	atc Ile	gaa Glu	ttt Phe 175	ctt Leu	528
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											gcc Ala 220					672
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atc Ile	agc Ser	gac Asp	gta Val 260	tcc Ser	gaa Glu	gct Ala	gcc Ala	gcc Ala 265	ege Arg	gcg Ala	cac His	acg Thr	ccg Pro 270	aaa Lys	gtc Val	816
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gtg Val	aat Asn 290	gcc Ala	gcc Ala	gac Asp	atc Ile	gat Asp 295	ttg Leu	ctg Leu	gta Val	cgc Arg	gcc Ala 300	ctg Leu	agc Ser	atg Met	ggc Gly	912
aaa Lys 305	ttg Leu	cac His	cac His	gcg Ala	atg Met 310	atg Met	ggt Gly	acc Thr	gcc Ala	tct Ser 315	gtt Val	gcc Ala	att Ile	gcg Ala	acc Thr 320	960
gcc Ala	gcc Ala	gcc Ala	gtg Val	Ccc Pro 325	ggt Gly	acg Thr	ctg Leu	gtc Val	aac Asn 330	ctt Leu	gcc Ala	gca Ala	ggc Gly	ggc Gly 335	gga Gly	1008
acg Thr	cgt Arg	Lys	gaa Glu 340	gtg Val	cgc Arg	ttc Phe	ggg	cat His 345	cct Pro	tcc Ser	ggc Gly	aca Thr	ttg Leu 350	cgc Arg	gtc Val	1056
ggt Gly	gca Ala	gcc Ala 355	gcc Ala	gaa Glu	tgt Cys	cag Gln	gac Asp 360	Gly	caa Gln	tgg Trp	acg Thr	gcc Ala 365	Thr	aaa Lys	gcg Ala	1104
gtt Val	atg Met 370	agc Ser	ege Arg	agc Ser	gca Ala	cgc Arg 375	gtg Val	atg Met	atg Met	Glu	ggt Gly 380	tgg (gtc a Val i	agg (gtg Val	1152
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Lys	Gly	Val	Phe 20	Phe	Lys	Arg	Ser	Asp 25	Leu	Pro	Glu	Ala	Ala 30	Arg	Glu
Ala	Gly	Ser 35	Ala	Arg	Asp	Lys	lle 40	Leu	Leu	Arg	Val	Leu 45	Gly	Ser	Pro
Asp	Pro 50	Tyr	Gly	Lys	Gln	Ile 55	Asp	Gly	Leu	Gly	Asn 60	Ala	Ser	Ser	Ser
Thr 65	Ser	Lys	Ala	Val	Ile 70	Leu	Asp	Lys	Ser	Glu 75	Arg	Ala	Asp	His	Asp 80
Val	Asp	Tyr	Leu	Phe 85	Gly	Gln	Val	ser	11e 90	Asp	Lys	Pro	Phe	Val 95	Asp
Trp	Ser	Gly	Asn 100	Cys	Gly	Asn	Leu	Thr 105	Ala	Ala	Val	Gly	Ala 110	Phe	Ala
Ile	Glu	Gln 115	Gly	Leu	Val	Asp	Lys 120	Gly	Lys	Ile	Pro	Ser 125	Asp	Gly	Ile
Cys	Thr 130	Val	Lys	Ile	Trp	Gln 135	Lys	Asn	Ile	Gly	Lys 140	Thr	Ile	Ile	Ala
His 145	Val	Pro	Met	Gln	Asn 150	Gly	Ala	Val	Leu	Glu 155	Thr	Gly	Asp	Phe	Glu 160
Leu	Asp	Gly	Val	Thr 165		Pro	Ala	Ala	Glu 170	. Val	Gln	Ile	Glu	Phe 175	Leu
Asp	Pro	Ala	Asp 180		Glu	Gly	Ser	Met 185		Pro	Thr	Gly	Asn 190		Val
Asp	Glu	Ile 195		Val	Pro	Asn	Ile 200		Arg	Leu	Lys	Ala 205	Thr	Leu	Ile
Asn	Ala 210		Ile	Pro	Thr	Val 215		Leu	Asn	Ala	Ala 220		Leu	Gly	Tyr
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<211> 389

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- Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu $_{245}$ $_{250}$ $_{255}$
- Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val \$260\$
- Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 275 280 285
- Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly 290 295 300
- Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr 305 \$310\$
- Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly 325 330 335
- Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val \$340\$
- Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala 355 360 365
- Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val 370 380

Pro Glu Asp Cys Phe 385

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<211> 2094

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- ott ota the age cae ata ggt ate gat the agt the att act ghe att. Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile

 35 40 45
- att tot gta tit atg gto ggo tig ggt gta ggt gog tat tit ggo gga 192 Tle Ser Vål Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
- cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Tle Pro Leu Phe Cys Ile

70

80

E A	ct q la (gaa g Blu	gta Val	tcc Ser	atc Ile 85	ggt Gly	ctg Leu	ttc Phe	ggt Gly	ttg Leu 90	gta Val	agc Ser	aag Lys	ggt Gly	ctg Leu 95	att Ile	288
t	er (ggc	Leu	999 Gly 100	cat Hıs	ctt Leu	tta Leu	gtt Val	gag Glu 105	gct Ala	gat Asp	ttg Leu	ccc Pro	atc Ile 110	atc Ile	get Ala	336
A A	ct q	Ala .	aat Asn 115	ttc Phe	ctc Leu	tta Leu	ttg Leu	ctg Leu 120	ctt Leu	cct Pro	acc Thr	ttt Phe	atg Met 125	atg Met	ggc Gly	geg	384
a T	hr :	ttg Leu 130	ecc Pro	ttg Leu	ctg Leu	acc Thr	tgt Cys 135	ttt Phe	ttt Phe	aac Asn	cgg Arg	aaa Lys 140	ata Ile	cat His	aat Asn	gtt Val	432
G	gc Ly 45	gag Glu	tct Ser	atc Ile	Gly	acc Thr 150	tta Leu	tat Tyr	ttt Phe	ttc Phe	aac Asn 155	act Thr	ttg Leu	ggt Gly	gcg Ala	gca Ala 160	480
Ţ	rc	gga Gly	tcg Ser	ctt Leu	gcc Ala 165	gcc Ala	gcc Ala	gaa Glu	ttt Phe	ttc Phe 170	tac Tyr	gtc Val	ttt Phe	ttt Phe	acc Thr 175	ctc Leu	528
S	ec	caa Gln	acc Thr	att Ile 180	gcg Ala	ctg Leu	aca Thr	gcc Ala	tgc Cys 185	ctt Leu	aac Asn	ctt Leu	ctg Leu	att Ile 190	gct Ala	gct Ala	576
t s	ca Ser	gta Val	tgc Cys 195	tgc Cys	gtt Val	aca Thr	gaa Glu	agg Arg 200	atg Met	gat Asp	atg Met	gtg Val	aac Asn 205	act Thr	aaa Lys	ccg Pro	624
i i	aat Asn	act Thr 210	agt Ser	gtg Val	att Ile	aat Asn	atg Met 215	ctt Leu	tct Ser	ttc Phe	ctt Leu	acc Thr 220	gga Gly	tta Leu	ttg Leu	agc Ser	672
1	ttg Leu 225	ggt Gly	ata Ile	gaa Glu	gtc Val	ttg Leu 230	Trp	gta Val	agg Arg	atg Met	ttt Phe 235	tcg Ser	ttc Phe	gca Ala	gca Ala	cag Gln 240	720
:	tcc Ser	gtg Val	cct Pro	cag Gln	gca Ala 245	ttt Phe	tca	ttt	att	ctt Leu 250	Ala	tgt Cys	ttt Phe	ctg Leu	acc Thr 255	Gly	768
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	gat Asp	ttt Phe 290	Leu	att Ile	ttg Leu	ggt	gct Ala 295	Ala	tgg Trp	ttg Lev	ttg Leu	acc Thr	Gly	ttt Phe	tcc Ser	ggt	912
	ttc Phe	gtc Val	cac His	cac His	gcc	ggt Gl	att	tto Phe	att	acc Thi	c cto r Lei	tct Se	gcc	gto Vai	gto Val	agg L Arg	960

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65

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gca Ala	ttg Leu	ggt Gly 355	ccg Pro	gtc Val	ctt Leu	atc Ile	ggc Gly 360	ttt Phe	gtg Val	ata Ile	ctt Leu	gat Asp 365	ttg Leu	ttg Leu	tcc Ser	1104
				tac Tyr												1152
				ctg Leu												1200
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				aat Asn												1296
				gtt Val												1344
				gta Val												1392
				atc Ile												1440
				att Ile 485												1488
				gcc Ala												1536
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cag Pro	ctt Leù 530	ttg Leu	cag Gln	gac	aaa Lys	cgt Arg 535	gtt Val	gaa Glu	att	gta Val	ttg Leu 540	Asp	gac Asp	ggt Gly	agg Arg	1632
															atg Met	1680

Jan.
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Page 1
220 23.00
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171
Call S
L

545					550					555					560	
aat Asn	tcg Ser	act Thr	tgg Trp	tac Tyr 565	tgg Trp	ogt Arg	gcc Ala	tat Tyr	tcc Ser 570	Thr	aac Asn	ctg Leu	ttg Leu	agt Ser 575	gcg Ala	1728
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agt Ser	att Ile 610	ccc Pro	tat Tyr	gca Ala	tac Tyr	cgc Arg 615	tac Tyr	Gly	cat	atg Met	gta Val 620	gtc Val	ggc Gly	tog Ser	gca Ala	1872
	ccg Pro															1920
	ttg Leu									Val						1968
	gat Asp								Ser							2016
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Phe	Ala	Ser	Gl 2		e C	rs A	la I	eu i	11e 25	Tyr	Gln	Val	Ser	Trp 30	Gln	Arg
Leu	Leu	Phe 35		r Hi	s II	Le G		le :	Asp	Leu	Ser	Ser	Ile 45	Thr	Val	Ile

The Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly 50 60 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile 65 75 80

70

Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile 85 90 95

Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala 100 \$105\$

Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala

Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val

Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala 145 \$150\$

Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu 165 170 175

Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala 180 185 190

Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro 195 200 205

Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser 210 220

Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln 225 230230235

Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly $245 \hspace{1cm} 255 \hspace{1cm}$

Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe $260 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$

Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala 275 280 285

Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly 290 295 300

Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg 305 310 315

Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys \$325\$

Ser Gly Arg Gln Val Ser Asn Val Tyr Fhe Ala Asn Val Ala Gly Ser $340 \ \ \, 345 \ \ \, 350$

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser 355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro 370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser 385 390 395 Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 415

Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn 420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val 435 440

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn 450 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala 485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala

Pro Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg 530 540

Lys Trp Leu Arg Arg his Pro Asp Glu Lys Phe Asp Leu Ile Leu Met S45 $$\,$ S50 $\,$ S55 $\,$ S60

Asn Ser Thr Trp Trp Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala 565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His 595 $\,$ 600 $\,$ 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala 610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser 625 630 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr $645 \hspace{1cm} 650 \hspace{1cm} 655$

Val Asp Ala Ala Ala Gin Lys Val Val Ser Arg Met Leu Ile Arg Met $660 \hspace{1.5cm} 665 \hspace{1.5cm} 670 \hspace{1.5cm}$

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(2237	ALCILICIAL	bequence description	. 1010	pramer
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Ş		5 5		
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	DNA	
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